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Sequence 69, Appl
Sequence 3209, Ap
Sequence 41, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
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11, Appl
40, Appl
10, Appl
14, Appl
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Sequence 1, Appli
Sequence 69, Appli
Sequence 61247, A
Sequence 126, App
Sequence 126, App
Sequence 832, App
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822, App
126, App
832, App
69, Appl
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Sequence 54, Appl
Sequence 824, App
                                                                                              February 22, 2006, 21:58:19; Search time 0.880829 Seconds (without alignments) 287.324 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2 6/ptodata/2/pubpāa/USO8 NEW PUB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*

8: /cgn2 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-106-932-11

US-11-106-932-11

US-11-106-755-09

US-11-045-024-14247

US-11-045-024-14247

US-11-043-039-032

US-11-106-932-69

US-11-106-932-69

US-11-174-816-43

US-11-174-816-43

US-11-174-816-41

US-11-072-51-11

US-11-072-1459-10

US-11-012-762-14
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US-11-012-762-18
US-11-012-762-20
US-11-012-762-24
US-11-012-762-40
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Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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94
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Match Length
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No.
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70, Appl 3821, Ap 3821, Appl 1062, Ap 1060, Ap 1050, Ap 1034, Ap 1034, Ap 1034, Ap 1037, Appl 21, Appl 10420, A 1058, Appl 21, Appl 22, Appli 6, Appli 6, Appli 7, Appli 10420, Appli 10420, Appli 6, Appli 7, Appli 10420, Appli Sequence Seq Sequence Seq Sequence Sequence Sequence Sequence Sequence US-11-106-932-70
US-11-072-512-310
US-11-072-512-310
US-10-714-887-32
US-10-453-372-1062
US-10-453-372-1066
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US-10-453-372-1054
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US-10-995-561-1034
US-10-995-561-1034
US-10-995-561-1034
US-10-995-561-1034
US-11-096-691-66
US-11-100-640-6
US-11-100-640-7 202 276 276 3100 3100 11798 3293 554 554 697 777 815 

### ALIGNMENTS

APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Rubo, Ralph
APPLICANT: Rubo, Ralph
APPLICANT: Epimmune Inc.
ITILE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
ITILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REPERENCE: 2006.004007
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REPERENCE: 2006.004007
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REPERENCE: 2006.004007
FILE REPERENCE: 2006.004007 OTHER INFORMATION: Standard Peptide 507.02 US-11-045-024-14523 Sequence 14523, Application US/11045024 ; Publication No. US20050271676A1 ; GENERAL INFORMATION: TYPE: PRT ORGANISM: Artificial Sequence US-11-045-024-14523

100.0%; Score 94; DB 7; Length 24; 100.0%; Pred. No. 1.6e-09;

Query Match Best Local Similarity

Sequence

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RESULT 6
US-11-150-755-69
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US-11-150-755-1
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LENGTH: 30
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Publication No. US2006002947a1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: HUMPHRENS:

APPLICANT: KU, MINZHEN

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/11/033,039

CURRENT PILING DATE: 2005-01-11

FRICR FILING DATE: 2005-01-11

FRICR FILING DATE: 2002-09-17

FRICR FILING DATE: 2002-09-17

FRICR FILING DATE: 1999-09-14

FRICR FILING DATE: 1999-09-14
                                                                                                                                                         RESULT 2
US-11-090-878-54
Sequence 54, Application US/11090878
Sequence 54, Application US/11090878
Publication No. US20050244911A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: Methods and Reagents for Identifying Compounds for TITLE OF INVERTION: Treating Autoimmune Disorders
TITLE OF INVENTION: Treating Autoimmune Disorders
CURRENT APPLICATION UNDER: US/11/090,878
CURRENT FILING DATE: 2005-03-25
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 94; DB 7; Length 197; Best Local Similarity 100.0%; Pred. No. 1.7e-08; Matches 17; Conservative 0; Mismatches 0; Indels
  0; Indels
  Mismatches
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Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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                                                                              6 ENPVOHFFKNIVTPRTP 22
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ORGANISM: Artificial Sequence
  17; Conservative
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US-11-033-039-824
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LENGTH: 197
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    Matches
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RESULT 4 US-11-106-932-11

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Sequence 11, Application US/11106932
Publication No. US20050260697A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WANG, KA-WANG KEVIN
APPLICANT: LIU, MING CHEN
APPLICANT: LIU, MING CHEN
APPLICANT: LIU, MING CHEN
APPLICANT: OLI, WONIKA
TITLE OF INVENTION: PROTECOLYTIC MAKKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
FILE REPERENCE: 5853-549-1
CURRENT FILING DATE: 2005-04-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: HERAPEUTIC PEPTIDES FOR DEMYELINATING CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/11/150, 755
CURRENT FILING DATE: 2005-06-10
PRIOR FILING DATE: 2002-12-09
PRIOR FILING DATE: 2001-01-29
PRIOR PLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1
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LOCATION: 85 - 99
OTHER INFORMATION: Immunodominant peptide of MBP, recognized by
CHER INFORMATION: HIA-DR2 haplotype
1.07HER INFORMATION: HIA-DR2 haplotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.8%; Score 83.5; DB 7;
94.4%; Pred. No. 1.1e-07;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/11150755; Publication No. US20060020109A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 ENPVVHFFKNIVTPPRTP 25
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Best Local Similarity 94.4
Matches 17; Conservative
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rattus rattus US-11-106-932-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 126, Application US/10893584

Publication No. US20050272048A1

GENERAL INFORMATION:

APPLICANT: Borgford, Thor

APPLICANT: Braun, Curtis

APPLICANT: Braun, Curtis

APPLICANT: Braun, Curtis

APPLICANT: Braun, Curtis

TITLE OF INVENTION: Viral or Parasitic Infections

TITLE OF INVENTION: Viral or Parasitic Infections

TITLE OF INVENTION: Viral or Parasitic Infections

FILE REFERENCE: 1047-025

CURRENT APPLICATION NUMBER: US 09/551,151

PRIOR FILING DATE: 2004-07-19

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 1999-10-29

PRIOR FILING DATE: 2000-10-04

NUMBER OF SEQ ID NOS: 274

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 126
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, OTHER INFORMATION: Mutant preproricin linker region for calpain, pAP-296
US-10-893-584-126
                                                                                                                                                                                                                                                                                                                                 | Sequence 822, Application US/11033039
| Publication No. US2006002947A1 |
| GENERAL INFORMATION: |
| APPLICANT: HUMPHREYS, ROBERT |
| APPLICANT: HUMPHREYS, ROBERT |
| APPLICANT: KU, MINZHEN |
| TITLE OF INVENTION: LI-EXY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES |
| TITLE OF INTENTION: LI-EXY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES |
| TILE REFERENCE: REH-2017US01 |
| CURRENT PILING DATE: 2005-01-11 |
| PRIOR PILING DATE: 2002-09-17 |
| PRIOR FILING DATE: 2002-09-17 |
| PRIOR FILING DATE: 1999-09-14 |
| ROBERT OF SEQ ID NOS: 1452 |
| SEQ ID NO 822 |
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        Mismatches
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ORGANISM: Artificial Sequence
                                                                                4 VVHFFKNIVTPRTP 17
        14; Conservative
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Best Local Similarity
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US-10-893-584-126
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        Matches
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APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Beteban
APPLICANT: Esteban
APPLICANT: Rubo, Ralph
APPLICANT: Rubo, Ralph
APPLICANT: Bpimmuno Inc.
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.004007
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.004007
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.004007
CURRENT FILING DATE: 1993-01-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR APPLICATION NUMBER: US 08/033,205
PRIOR PILING DATE: 1993-03-05
PRIOR PILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR PILING DATE: 1993-11-29
PRIOR PILING DATE: 1993-11-29
PRIOR PILING DATE: 1993-11-29
PRIOR PILING DATE: 1994-03-04
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TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING CONDITIONS
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CHER INFORMATION: The peptide was designed and synthesized.
US-11-150-755-69
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                                FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/11/150,755
CURRENT FILING DATE: 2005-06-10
FRIOR APPLICATION NUMBER: US/10/056,583
FRIOR FILING DATE: 2002-12-09
FRIOR FILING DATE: 2002-12-09
FRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PATENTIN VET: 2.1
SOFTWARE: PATENTIN VET: 2.1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14247
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14247, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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GARLEAU INCOCKATION:
APPLICANT: EBELING:
APPLICANT: HOENER, MARIUS
APPLICANT: HOENER, MARIUS
TITE CONTINUENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS
FILE REFERENCE: 22645
CURRENT APPLICATION NUMBER: US/11/174,816
CURRENT APPLICATION NUMBER: US/11/174,816
CURRENT APPLICATION NUMBER: EP 04103261.6
PRIOR APPLICATION NUMBER: EP 04103261.6
PRIOR FILING DATE: 2004-07-08
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PATENTION VERSION 3.3
SEQ ID NO 4: PATENTION VERSION 3.3
TENET PRIOR PILING SECTION NOS: 115
SOFTWARE: PATENTION NOS: 115
TYPE: PRI
TYPE: PR
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Best Local Similarity 26.7%; Pred. No. 33;
Matches 8; Conservative 5; Mismatches 3; Indels
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR PELLING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2001-11-05
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                      ; Sequence 3209, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
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US-11-174-816-43
Sequence 43, Application US/11174816
Publication No. US2006009441A1
GENERAL INFORMATION:
                                                                                                                                                      APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZIKO
APPLICANT: ISHII, SHIZIKO
APPLICANT: ISHII, SHIZIKO
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| :| : |||||
533 ESPRIHPTRIPKTPRTP 549
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAMECHIKA, ICHIRO
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3209
LENGTH: 574
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IRIE, RYOTARO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-072-512-3209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAGAI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
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) Sequence 69, Application US/11106932
) Sequence 69, Application US/11106932
) Sequence 69, Application US/11106932
) Sequence 69, Application Occupant Occu
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| Sequence 812, Application US/11033039
| Publication No. US20060002947A1
| GENERAL INFORMATION:
| APPLICANT: HUMPHREXS, ROBERT
| APPLICANT: HUMPHREXS, ROBERT
| APPLICANT: W. MINZHEN
| TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| FILE REFERENCE: REH-2017US01
| CURRENT PAPLICATION NUMBER: 10/245,871
| PRIOR PLILING DATE: 2005-01-11
| PRIOR PLILING DATE: 2002-09-17
| PRIOR PLILING DATE: 2002-09-17
| PRIOR PLILING DATE: 2002-07-17
| PRIOR PLILING DATE: 1002-07-17
| PRIOR PLILING DATE: 1995-09-14
| NUMBER OF SEQ ID NOS: 1452
| SEQ ID NO 832
| LENGTH: 9
Gaps
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    Indels
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Pred. No. 8.3e+04;
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Mismatches
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0
11; Conservative
                                                                                                                                         1 FFKNIVTPRTP 11
                                                                                    7 FFKNIVTPRTP 17
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US-11-106-932-69
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US-11-033-039-832
    Matchee
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                                                                                                                                                          Sequence 11, Application US/11174819
Publication No. US2006000880A1
GENERAL INFORMATION
APPLICANT: BELING, MARTIN
APPLICANT: HORBER, MARIUS
TITLE OF INVENTION: POURSE TRACE AMINE ASSOCIATED RECEPTORS AND
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/11/174,819
CURRENT APPLICATION NUMBER: EP 04103262.4
PRIOR APPLICATION NUMBER: P 04103262.4
PRIOR FILING DATE: 2004-07-08
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.3
SEQ ID NO 11
LENGTH: 337
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| Sequence 40, Application US/11075046
| Publication No. US20050268353A1
| Publication No. US2005026835A1
| GENERAL INFORMATION:
| APPLICANT: P. D. CHRISTIAN, K. H. J. GORDON and
| APPLICANT: T. N. HANZLIK
| TITLE OF INVENTION: INSECT VIRUSES AND THEIR USES IN
| TITLE OF INVENTION: PROTECTING PLANTS
| NUMBER OF SEQUENCES: 53
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: PORSEY & WHITNEY LLP
| STREET: FOUR EMBARCADERO CENTER, SUITE 3400
| CITY: SAN FRANCISCO
| STATE: CALIFORNIA
| COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAttentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/075,046
FILING DATE: 07-MAR-2005
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APPLICATION NUMBER: US/09/677,653
FILING DATE: 03-0ct-2000
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD F. TRECARTIN
REFIRENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC
                           301 NPIIYVFSYRWFRKALKLLLSREIFSPRTP 330
2 NPVVHFF-----KNIVTPRTP 17
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US-11-174-819-11
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ORGANISM: Mus musculus
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US-11-174-819-11
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RESULT 2
US-10-000-439-13

i Sequence 13, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: SAXON, Andrew
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFRENCE: UCG77.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR SEQ ID NOS: 13
; NUMBER OF SEQ ID NOS: 13
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Best Local Similarity
Matches 17; Conserv
US-10-104-973-3
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 TYPE: PRT
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Sequence 8, Appli
Sequence 1, Appli
Sequence 4219, Ap
Sequence 4219, Ap
Sequence 4219, Ap
Sequence 326, App
Sequence 2501, App
Sequence 2501, App
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30, Appl
35, Appl
49, Appl
26, Appl
11, Appli
11, Appli
8, Appli
11, Appli
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                                                            February 22, 2006, 21:57:24; Search time 8.69085 Seconds (without alignments) 817.308 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, App
Sequence 6, App
Sequence 1, App
Sequence 12, App
Sequence 143, App
Sequence 28, App
Sequence 28, App
Sequence 39, App
Sequence 49, App
Sequence 26, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                     Published Applications AA Main: * /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: * ; /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * ; /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: * ; /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep: * ; /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: * ; /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: * ; /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-300-439-13

US-10-233-892A-2

US-10-233-892A-2

US-10-740-013-6

US-10-740-003-2

US-09-766-378A-32

US-09-766-378A-28

US-09-76-378A-28

US-09-836-433-30

US-09-836-433-30

US-09-859-012-35

US-09-859-012-35

US-09-859-012-35

US-09-859-012-35

US-09-892-40-1

US-09-90-46-1

US-09-90-46-1

US-09-90-46-1

US-09-90-46-1

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-10-149-138-4219
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US-10-654-601-2501
US-11-051-411-1220
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                  1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                  US-10-000-439-13
94
1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                        Scoring table:
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                                                                                                                       Seguence:
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No.
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Sequence 1, Appli
Sequence 1, Appli
Sequence 115, Appli
Sequence 339675,
Sequence 12, Appli
Sequence 2, Appli
Sequence 12, Appli
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Sequence 3, Application US/10104973

Publication No. US20020176866A1

GENERAL INPORMATION:

APPLICANT: Gaur, Amitabh

APPLICANT: Ling, Nicholas C.

APPLICANT: Ling, Nicholas C.

APPLICANT: Ling, Nicholas C.

TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING

TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING

TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING

TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING

TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING

TITLE OF INVENTION WINBER: US/10/104,973

CURRENT APPLICATION NUMBER: US/10/104,973

SOFTWARE: PACEULIN Ver. 2.0

SEQ ID NOS: 8

SECTION OS: 8

SECTION OS: 8
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                                                                                                                                                                           Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1
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  US-09-813-183-1
US-09-813-463A-1
US-09-813-463A-1
US-10-492-794-115
US-10-425-115-339675
US-10-475-1104-32
US-10-126-894B-1
US-10-199-995-3
US-10-199-995-3
US-09-989-476-2
US-10-104-973-2
US-110-000-439-12
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Gaps

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US-10-465-04-10

Subjection No. US20040235713A1

Subjection No. US20040235713A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE REFERENCE: 2749 FPMO

TITLE OF INVENTION:

TIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-770-712-6

Sequence 6, Application US/10770712

Sequence 6, Application US/10770712

Publication No. US20050170333A1

GENERAL INFORMATION:

TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM

FILE REFERENCE: IMSCI2.008A

CURRENT APPLICATION NUMBER: US/10/770,712

CURRENT FILING DATE: 2004-02-03

NUMBER OF SEQ ID NOS: 133

SOCHWARE: FaetSEQ for Windows Version 4.0

LENGTH: 17
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                   100.0%; Score 94; DB 4; Length 17; 100.0%; Pred. No. 5.3e-08; ive 0; Mismatches 0; Indels
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100.0%; Score 94; DB 5; Sest Local Similarity 100.0%; Pred. No. 5.3e-08; Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: glycopeptide
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Query Match
Best Local Similarity 100..
Best 17; Conservative
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Best Local Similarity 100.0
Matches 17; Conservative
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US-10-482-044-5
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LENGTH: 17
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100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                 Query Match

100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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Publication No. US200400431A1

GENERAL INFORMATION:

APPLICANT: Voldani, Arieto

TITLE OF INVENTION: DIAGNOSIS OF MULTIPLE SCLEROSIS AND

TITLE OF INVENTION: OTHER DEMYELINATING DISEASES

TILE REFERENCE: INSNS. OOLA

CURRENT APPLICATION NUMBER: US/10/233,892A

CURRENT AILING DATE: 2002-08-29

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-362-264-1
Sequence 1, Application US/10362264
Publication No. US20030191063A1
GENERAL INPORMATION:
APPLICANT: Wraith, David
APPLICANT: Maza, Graziella
APPLICANT: Ponsford, Mary
APPLICANT: Ponsford, Mary
APPLICANT: Ponsford, Mary
APPLICANT: The University of Bristol
TITLE OF INVENTION: PEPTIDE SELECTION METHOD
FILE REFERENCE: 1433.004USI
CURRENT APPLICATION NUMBER: US/10/362,264
CURRENT APPLICATION NUMBER: OGS-21
FILE REFERENCE: 12001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-17
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                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-439-13
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   SEQ ID NO 13
LENGTH: 17
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PRIOR FILING DATE: 1999-03-09
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Matches 17; Conserv
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APPLICANT: Arnon, Ruth
APPLICANT: Sela, Michael
APPLICANT: Sela, Michael
APPLICANT: Strominger, Jack
TITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer 1
TITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer 1
TITLE OF INVENTION: and Related Copolymers and Peptides
FILE REFERENCE: 1662/493768,872
CURRENT APPLICATION NUMBER: US 60/093,859
PRIOR APPLICATION NUMBER: US 60/101,825
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: US 60/102,960
PRIOR APPLICATION NUMBER: US 60/106,350
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: US 60/106,350
PRIOR APPLICATION NUMBER: US 60/106,350
PRIOR APPLICATION NUMBER: US 60/106,350
PRIOR APPLICATION NUMBER: US 60/102,960
PRIOR APPLICATION NUMBER: US 60/106,350
PRIOR APPLICATION NUMBER: US 60/102,960
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GENERAL INFORMATION:
APPLICANT: RAYCHAUDHUR, SYAMAL
APPLICANT: BLACK, AMELIAM
ITILE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
FILE REFERENCE: 37003/275802
CURRENT APPLICATION NUMBER: US/09/740,003
CURRENT APPLICATION NUMBER: US/09/24,220
PRIOR APPLICATION NUMBER: 08/476,674
PRIOR APPLICATION NUMBER: 08/476,674
PRIOR FILING DATE: 1995-06-07
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/351,001
PRIOR FILING DATE: 1997-08-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                     Sequence 2, Application US/09740003 Publication No. US20020039582A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09768872
Patent No. US20020055466A1
GENERAL INFORMATION:
APPLICANT: Abaroni, Rina
APPLICANT: Teitelbaum, Dvora
1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ENPVOHEFKNIVIPRIP 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-740-003-2
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US-09-768-872-1
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Gaps
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ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                 Query Match
100.0%; Score 94; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                            ; OTHER INFORMATION: synthetic peptide (MBP residues 84-102) US-09-768-872-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acevedo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES P
METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 48002-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/766,378A FILING DATE: 19-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-766-378A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,190
FILING DATE: 29-OCT-1997
NUMBER OF SEQ ID NOS: 3
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 1
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/09766378A Patent No. US20020091079A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: usa
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                 ENPVVHFFKNIVTPRTP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rhode, Peter R.
                                                                                                                                                                                                                                                                                                                                 1 ENPVWHEFKNIVTPRTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 32
                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Gaps
                                                                                                                                                     Gaps
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: peptide US-10-743-398-2
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                      Length 19;
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                                                                                                                                                     0; Indels
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ZIP: 02109

COMPUTER: Usa

COMPUTER: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSED for Windows Version 2.0

SOFTWARE: FastSED for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,378A

FILING DATE: 19-Jan-2001

CLASSIFICATION: CURNOwn>
PRIOR APPLICATION SOFTWARE: 08/960,190

FILING DATE: 29-OCT-1997

ATTORNEY/AGNT INFORMATION:

NAME: COF1889, Peter F

REGISTRATION NUMBER: 33,860

REFERENCE/DOCKET NUMBER: 33,860

TELECOWNUNICATION INFORMATION:

TELECOWNUNICATION INFORMATION:

TELECOWNUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acevedo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C. MHC COMPLEXES AND
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 94; DB 3; 100.0%; Pred. No. 6.4e-08; tive 0; Mismatches 0;
                                                                                                 100.0%; Score 94; DB 4;
100.0%; Pred. No. 6e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-766-378A-28
                                                                                                                                                                                                                                                                                                                                        US-09-766-378A-28
; Sequence 28, Application US/09766378A
; Patent No. US20020091079A1
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ENPWHFFKNIVTPRTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                   1 ENPVWHEFKNIVTPRTP 17
                                                                                                                                                                                                                                                2 ENPVVHFFKNIVTPRTP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
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                                                                                                           RESULT 10
US-10-239-313A-143
is Sequence 113, Application US/10239313A
is Sequence 113, Application US/2030175285A1
is Dublication No. US20030175285A1
is Dublication No. US20030175285A1
is Dublication No. US20030175285A1
is Dublication No. US20030175285A1
is APPLICANT: KINGUEN - HAMOUR, Christine
is APPLICANT: CORVAIA, Nathalie
is APPLICANT: GOETSCH, Ialiane
is TITLE OF INVENTION: MULECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
it IE REPERENCE: 343 727 - US
it IE REPERENCE: 343 727 - US
it CURRENT FILING DATE: 2002-09-19
is PRIOR FILING DATE: 2002-09-19
is PRIOR FILING DATE: 2000-03-23
is PRIOR PELICATION NUMBER: PCT 01/7072
is SOFTWARE: Patentin Ver. 2.1
is SEQ ID NO 143
in LENGTH: 19
in LENGTH: 19
in LENGTH: 19
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Sequence 2, Application US/10743398

Publication No. US20040197331A1

GENERAL INFORMATION:
APPLICANT: RAYETHURIN, SYAWAL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: BLACK, AMELIA
ITILE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
ITILE REPERENCE: 37003/307430
CURRENT APPLICATION NUMBER: US/10/743,398
CURRENT PILING DATE: 2003-12-23
FRIOR FILING DATE: 1998-02-17
FRIOR PILING DATE: 1998-02-17
FRIOR APPLICATION NUMBER: 09/024,220
FRIOR APPLICATION NUMBER: 09/024,220
FRIOR APPLICATION NUMBER: 09/1476,674
FRIOR APPLICATION NUMBER: 08/351,001
FRIOR APPLICATION NUMBER: 08/319,787
FRIOR APPLICATION NUMBER: 07/735,069
FRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN Ver. 2.1
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                                         1 ENPVOHEFKNIVTPRIP 17
                                                                    1 ENPVVHEFKNIVTPRTP 17
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RHODE, PETER
APPLICANT: WITTMAN, VAUGHAN
APPLICANT: WITTMAN, VAUGHAN
APPLICANT: WITTMAN, VAUGHAN
APPLICANT: WITTMAN, JON A.
APPLICANT: GARD, KIMBERLYN F.
APPLICANT: TAL, RONY
APPLICANT: TAL, RONY
APPLICANT: ACEVEDO, JONGE
APPLICANT: ACEVEDO, JONGE
APPLICANT: WONG, HING C.
TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS
FILE REFERENCE: 49444 (11758)
CURRENT APPLICATION NUMBER: US/09/859,012
CURRENT APPLICATION NUMBER: 60/206,920
FRIOR FILING DATE: 2001-05-16
FRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 35
INDERTHED TO 35
INDERTHED TO 35
INDERTHED TO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 94; DB 3; Length 20; 100.0%; Pred. No. 6.4e-08;
                 Sequence 30, Application US/09836433
Publication No. US20030049797A1
GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigazu
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REPERENCE: No. US20030049797A1 Assigned
CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DACE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
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Publication No. US20040253632A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49, Application US/09859012; Publication No. US20040253632A1; GENERAL INFORMATION: PETER APPLICANT: HIODE, PETER APPLICANT: WITTMAN, VAUGHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ENPVYHFFKNIVTPRTP 19
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                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: synthetic construct
US-09-836-433-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Matches 17; Conservative
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US-09-859-012-49
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US-09-859-012-35
US-09-836-433-30
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LENGTH: 20
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## APPLICANT: WEIDANZ, JON A.

## APPLICANT: BURKHARDY, MARTIN

## APPLICANT: BURKHARDY, MARTIN

## APPLICANT: BURKHARDY, MARTIN

## APPLICANT: TAL, RONY

## APPLICANT: APPLICANTON

## APPLICANT: APPLICANTON

## APPLICANT: APPLICANTON

## APPLICANT: MONG, HING C.

## TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS

## TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS

## TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS

## TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS

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## TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS

## TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS

## TITLE OF INVENTION WOMBER: 60/206,920

## TITLE OF INVENTION OF T CELL RECEPTOR INTERACTIONS

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## OF TITLE OF INVENTION OF T CELL RECEPTOR INTERACTIONS

## OF TITLE OF INTERACTIONS

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                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
Query Match
Best Local Similarity
Matches 17; Conserv
RESULT 1
US-09-137-759-3
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Sequence 18, Appli
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Sequence 17, Appli
Sequence 24, Appli
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                                                     February 22, 2006, 21:37:34 ; Search time 2.52504 Seconds
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Sequence 46,
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        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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/cgn2_6/prodata/1/iaa/6_COMB.pep:*
/cgn2_6/prodata/1/iaa/FCTUS_COMB.pep:*
/cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/prodata/1/iaa/RE_COMB.pep:*
/cgn2_6/prodata/1/iaa/RE_COMB.pep:*
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US-08-640-344-2
US-08-640-344-2
US-08-468-540B-9
US-08-468-540B-24
US-08-297-395-1
US-08-960-190A-32
US-08-449-728-2
US-08-449-728-2
US-08-449-728-2
US-08-640-344-3
US-08-640-344-4
US-08-640-344-6
US-08-640-344-6
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US-09-239-043D-2501
                                                                                                                                                          Fotal number of hits satisfying chosen parameters:
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PCT-US93-07545-46
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3-08-640-344-6
3-08-640-344-7
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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
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                                                                                     US-10-000-439-13
94
1 ENPVVHFFKNIVTPRTP 17
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                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Patent No. 5194425
Sequence 1, Appli
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Sequence 3, Application US/09137759

Patent No. 6251396

GENERAL INFORMATION

APPLICANT: Gaur, Amitabh

APPLICANT: Gaur, Amitabh

APPLICANT: Conlon, Paul J.

APPLICANT: Ling, Nicholas C.

APPLICANT: Staehlin, Theophil

APPLICANT: Staehlin, Theophil

APPLICANT: Staehlin, Theophil

TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING

TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN

TITLE OF INVENTION NUMBER: US/09/137,759

CURRENT FILING DATE: 1998-08-20

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 8

SEQ ID NOS: 8

SEQUENCE: Applicant Number OF SEQ ID NOS: 8
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US-09-378-244-3
; Sequence 3, Application US/09378244
; Patent No. 6379670
; GENERAL INFORMATION:
; APPLICANT Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Staehlin, Theophil
; TITLE OF INVENTION: PETTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; TITLE OF INVENTION PETTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; TILE REFERENCE: 690068-405622
; CURRENT APPLICATION NUMBER: US/09/378,244
; CURRENT FILING DATE: 1999-08-19
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5194425-4

US-08-227-372-1

US-08-327-372-1

US-08-470-397-1

US-09-007-520-1

US-09-055-263-1

US-09-055-263-1

US-09-055-263-1

US-09-055-263-1

US-09-055-263-1

US-09-017-259-1

US-09-137-759-2

US-09-137-759-2

US-09-989-476-2

US-09-989-476-2
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RESULT 5
US-08-468-540B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weiner, Howard
APPLICANT: Hafler, David
APPLICANT: Miler, Ariel
APPLICANT: Al-Sabgh, Ahmad
APPLICANT: Al-Sabgh, Ahmad
TITLE OF INVENTION: GING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence: Solid Phase; OTHER INFORMATION: Synthesis
US-09-378-244-3
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                                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                          Query Match 100.0%; Score 94; DB 2; I
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN 1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-468-540B-18; Sequence 18, Application US/08468540B; Patent No. 5858980; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                            1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                     1 ENPVVHFFKNIVTPRTP 17
                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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COUNTRY: US
ZIP: 10022
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1 ENPVOHFFKNIVTPRTP 17

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APPLICATION NUMBER: US/08/468,540B FILING DATE: 06-JUN-1995 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: ATTORNEY, AGENT INFORMATION: NAME: Jacobs, Seth H REGISTRATION NUMBER: 32,140
                                                                                    INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 5858980e
            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acide
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TOPOLOGY: linear
MOLECULE TYPE: No. 5858980e
US-08-468-540B-24
                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 17; Conservative
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amino acid
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US-08-468-540B-24
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       ZIP: 10022
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DISKETED
COFTWARE: PASTSRO for Windows Version 2.0
SOFTWARE: PASTSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: ACODS, SETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08468540B Patent No. 5858980
                                                                                                                                                                                                                    NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ENPVVHFFKNIVTPRTP 18
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                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: No. 5858980e
                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-468-540B-17
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; Patent No. S858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Miller, Ariel
; APPLICANT: Miller, Aniel
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
                                                           Gaps
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100.0%; Score 94; DB 1; Length 19; 100.0%; Pred. No. 8e-09; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDLIN TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRESESO for Windows Version 2.0
APPLICATION NUMBER: US/08/468,540B
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Gaps
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APPLICANT: Aceved, Jorge
APPLICANT: Aceved, Jorge
APPLICANT: Jiao, Jin-an
APPLICANT: Jiao, Jin-an
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                                                                                           APPLICATION NUMBER: US 07/919,787
FILING DATE: 24-JUL-1992
APPLICATION NUMBER: US 07/735,069
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-149
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1896-6620
TELECOMMUNICATION 1896-6620
TELECOMMUNICATION 1896-6620
TELECOMMUNICATION 1997-6201
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 29-0CT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 94; DB 2; Best Local Similarity 100.0%; Pred. No. 8e-09; Matches 17; Conservative 0; Mismatches 0
                                                                         APPLICATION NUMBER: 08/476,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-960-190A-32
; Sequence 32, Application US/08960190A
; Patent No. 6232445
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 19 amino acide
TYPE: amino acid
STRANDEDNESS: single
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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NAME: Corless, Peter F
REGISTRATION NUMBER: 33,
                                                PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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ZIP: 02109
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Patent No. 6197311
GENERAL INFORMATION:
APPLICANT: RAXCHAUDHURI, Syamal
RASTETTER, William H.
BLACK, Amelia
TITLE OF INVENTION INDUCTION OF CYTOTOXIC T-LYMPHOCYTE
RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Burne, Doane, Swecker & Mathis STREET: B. o. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,220
FILING DATE: 17-Feb-1998
CLASSIFICATION: «Unknown»
Z1-JUL-1992
                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08297395A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
APPLICANT: Howard L. Weiner
APPLICANT: David A. Hafler
ITILE OF INVENTION: EPETIDES DERIVED FROM IMMUNODOMINANT
ITILE OF INVENTION: EPETIDES OF WYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3
CURRENT APPLICATION NUMBER: 08/059,189
EARLIER FILING DATE: 1993-05.06
EARLIER APPLICATION NUMBER: 07/502,559
EARLIER PILING DATE: 1990-03-30
EARLIER PILING DATE: 1990-03-30
EARLIER PILING DATE: 1980-06-24
EARLIER FILING DATE: 1988-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 94; DB 2; Length 19; 100.0%; Pred. No. 8e-09; tive 0; Mismatches 0; Indels
                                                     Indels
Pred. No. 8e-09;
Best Local Similarity 100.0%; Pred. No. 8e-
                                                                                                                                    2 ENPVYHEFKNIVTPRTP 18
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COGANISM: Homo sapiens
US-08-297-395-1
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Best Local Similarity
Matches 17; Conserv
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US-09-024-220-2
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APPLICANT: EVELINE BERAUD
APPLICANT: RINA MARIANOVSKY
APPLICANT: RINA MARIANOVSKY
APPLICANT: RINA MARIANOVSKY
TITLE OF INVENTION: PSEUDOMONAS EXOTOXIN-MYELIN BASIC PROTEIN CHIMERIC
FILE REFERENCE: LOREBERBOUM=1
CURRENT APPLICATION NUMBER: US/09/077,028A
CURRENT PILING DATE: 1995-05-18
PRIOR APPLICATION NUMBER: IL11659
PRIOR PLING DATE: 1995-11-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SSEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09740003
Fatent No. 6733763
Fatent No. 6733763
GENERAL INFORMATION:
APPLICANT: RAYCHAUDHURI, SYAMAL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: BLACK, AMELIA
TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
FILE REFERENCE: 37003/275802
CURRENT APPLICATION NUMBER: US/09/740,003
CURRENT FILING DATE: 12998-02-17
PRIOR PILING DATE: 1998-02-17
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/919,787
PRIOR PILING DATE: 1991-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: peptide US-09-740-003-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 94; DB 2; Length 19;
100.0%; Pred. No. 8e-09;
cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8e-09;
tive 0; Mismatches 0; IndelB
                                           Sequence 15, Application US/09077028A Patent No. 6531133 GENERAL INFORMATION: APPLICANT: HAYA LORBERBOUM-GALSKI APPLICANT: IDA STEINBERGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ENPVVHFFKNIVTPRTP 17
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
Matches 17; Conserva
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Matches 17; Conserv
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Query Match

Best Local Similarity 100.0%; Pred. No. 8e-09;

Matches 17; Conservative 0; Mismatches 0; Indels
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Pred. No. 8e-09;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: SYAVAL ENCHAUDHURI
APPLICANT: WILLIAM H. RASTETTER
TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08449728 Patent No. 6270769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J.
REGIGSTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 194/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%;
Matches 17; Conservative 0,
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TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: protein
US-08-960-190A-32
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STRANDEDNESS: single
TOPOLOGY: linear
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TOPOLOGY:
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US-00-640-344-1

i Sequence 1, Application US/08640344

i Patent No. 5824315

GENERAL INFORMATION:

APPLICANT: MAG, BISHWAJIT

APPLICANT: MIKKU, PRABHA

TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC

TITLE OF INVENTION: PEPTIDES FOR WHC MOLECULES

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TWO BRHARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111-334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IPAM PC COMPALIBLE

COMPUTER: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATH:

CLASSIFICATION NUMBER: US/08/640,344

FILING DATE: 30-DANMINGN.
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Patent No. 5824315

GENERAL INFORMATION:
APPLICANT: MUKKU, PRABHA

APPLICANT: DESHPANDE, SHRIKANT

ITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC

ITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TOWNSEND & TOWNSEND & TOWNSEND
CITY: SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/ACENT INFORMATION:
NAME: STORELLA ESO., JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
                            2 ENPVVHFFKNIVTPRTP 18
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ENPVVHEFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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COUNTRY: U.S.A.

ZIP: 94111-3834

COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPER FLOWERDED
CONTRANT SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,344
FILING DATE: 30-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA ESO., JOHN R.
REGISTRANCE/DOCKET NUMBER: 32,94
FELEPAN: (415) 576-020
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION:
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NCBI_TaxID=9606;
Name=Mbp;
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equus cabal
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mus musculu
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homo sapien
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carcharhinu
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                                         February 22, 2006, 21:24:24; Search time 11.304 Seconds
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Q5nvg4
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Q5NVG4_PONPY
Q54ZT4_MOUSE
Q8R4K6_RAT
Q6F104_HUMAN
Q6F104_HUMAN
Q5R7J4_PONPY
MBP_CAVPO
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OGJ2R3 PIG
OGPK23 HUMAN
MBP RAT
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MBP HUMAN
MBP HUMAN
MBP CHICK
OS 1012 GECJA
OS 6972 XENLA
MBP XENLA
MBP XENLA
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MBP XENLA
MBP XENLA
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QSIZC7_BRARE
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
                                                                 US-10-000-439-13
94
1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                   MBP.
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                                                                                                                                                                              UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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304
173
                                                                                                                                                                                                                                                                   Scoring table:
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                                                                       Perfect score:
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                                                                               Sequence:
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                                          Run on:
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32 51 54.3 516 2 QSWTL4_LBGPL Q86i29 dictyostelia  
33 49.5 52.7 668 2 Q86i29_DICDI Q86i29 dictyostelia  
34 49 52.1 516 2 QSXIV3_LBGPA Q86i29 dictyostelia  
35 47 50.0 2 QS33W5_ENTPA Q833W5_ENTPA  
36 47 50.0 516 2 QS2BD2_LBGPH Q52ad2 legionella  
37 47 50.0 669 2 QSBB7_ERWCT Q66dB7 erwinia car  
38 46 48.9 233 2 Q60B7_CRER Q66dB7 erwinia car  
40 46 48.9 233 2 Q60B7_CRER Q66dB7 erwinia car  
41 46 48.9 439 2 Q4Z5T7_PSESY Q884d3 pseudomonas  
42 46 48.9 1529 2 QADAJG_LBIMA Q72xi2 xenopus lae  
43 46 48.9 1529 2 QADAJG_LBIMA Q72xi2 xenopus lae  
44 45 47.9 315 2 Q4H5F9_9DBIO Q4H5F9 deinococcus
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# ALIGNMENTS

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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp68610845 (Fragment).
Name-DKFZp68610845,
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ottenwaelder B., Obermaler B., Deutschenbaur S., Schaipp A.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann submitted (KUG-2004) to the BMBL/GenBank/DDBJ databases.
BMBL, CR627018; CAH10359.1; -; mANA.
GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
InterPro; IFR000648; Myelin BP.
ProDom; PF01669; Myelin BP; 1.
PRODOM; PD004542; Myelin BP; 1.
PROSITE; PS016569; MYELIN MBP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 AA; 8265 MW; ACFE96ACBE9AE551 CRC64;
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Last annotation update)
74 AA
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PRT;
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050501;
13-SEP-2005 (TrEMBLrel. 31, Cr
13-SEP-2005 (TrEMBLrel. 31, La
13-SEP-2005 (TrEMBLrel. 31, La
Myelin basic protein.
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                                              25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                      VICLEOTIDE SEQUENCE.
TISSUE=Amygdala;
The German CDNA Consortium;
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NUCLEOTIDE SEQUENCE
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                                                                                Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rianener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleron M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Widnin T.B., Toobhyuki S., Carninci P., Frange C.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Wilting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

M. Hiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Schnerch A., Schehu J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Fobo G., Han M., Wiemann S.;

Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR926072; CAI29699.1; -; mRNA.

EMBL; CR926072; CAI29699.1; -; mRNA.

EMBL; PF016911; F: Structural constituent of myelin sheath; IEA.

InterPro; IPR000548; Myelin BP.

Pfam; PF01669; Myelin MBP; I.

PRINTS; PR00212; MYELINMBP.
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                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BC094522, AAH94522.1; -; mRNA.
InterPro; IRN00584; Myelin BP.
Pfam; PF01669; Myelin MBP; I.
PRINTS; PR00212; MYELINMBP.
Prodom; PD004542; MyeLin BP; 1.
SEQUENCE 128 AA; 1421I MM; 2DAF033C19CF111C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
10-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp459G2410.
Name=DKFZp459G2410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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QSNVG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
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TISSUE=Brain;
                     NUCLEOTIDE SEQUENCE.
TISSUE=Brain;
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ACCOUNTINGENTIAL SEQUENTS.

AND INTEGRATIAL SEQUENTS.

A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S., Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H., Kadota K., Matsuda H.A., Staubir F., Saito T., King B., Kochiwa H., Rabischmann W., Casaterland T., Gissi C., King B., Kochiwa H., Rabischmann W., Staubir F., Suzuki R., Tomital M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M., Arometelli S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Ringwald M., Rodriguez I., Sakamoto N., Schoch K.-F., Sakanich M., Sato K., Schoenbach C., Schoenbach C., Schoenbach C., Schoenbach C., Schoenbach C., Whittaker C., Wilming L., Mynchaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Winnershav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRAIN=C57BL/6J; TISSUE=Spinal cord;
MEDLINE=22354681; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=22354681; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kaukwawa T., Adachi J., Bono H., Kondo S., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Sadiarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dallas E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Garriboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-58P-2005 (TrEMBLrel. 31, Created)
13-58P-2005 (TrEMBLrel. 31, Last sequence update)
13-58P-2005 (TrEMBLrel. 31, Last annotation update)
Adult male spinal cord cDNA, RIKEN full-length enriched library,
clone:A330079E24 product:myelin basic protein, full insert
                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                         Score 94; DB 2; Length 150;
Pred. No. 2.1e-07;
; Mismatches 0; Indels
PROSITE; PS00569; MYELIN_MBP; 1.
Hypothetical protein.
SEQUENCE 150 AA; 16277 MW; AF41CBDB96D8FD01 CRC64;
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                                                                                                                                                                                  Query Match
100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
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Q542T4;
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                         Konagaya A., Kurochki, Lee Y., Cenhard B., Lyons P.A.,
A Magabima T., Martais L., Marchionni L., McKenzie L., Miki H.,
A Magabima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesele G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Serou M., Shimada K.,
A Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watnabe Y., Wells C.,
A Wilning L.G., Whyshaww Boris A., Carninci P., Hayatsu N.,
A Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
A Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
A Bhraai T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
A Hara A., Hashizume W., Imotani K., Sasaki D., Shibata K., Shinagawa A.,
A Funnishi A., Yoshino W., Waterston R., Lander E.S., Rogers J.,
B Franck F. Harashi, V., Sasaki D., Shibata K., Lander E.S., Rogers J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
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Pred. No. 2.2e-07;
Mismatches 0; Indels
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SEQUENCE 154 AA; 17225 MW; 00F1F10ECF90421B CRC64;
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STRAIN-CS7BL/6J; TISSUE-Spinal cord;
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MGI; MGI:96925; Mbp.
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100.0%; Pre-
0; '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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Matches
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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MEDINE=2294925; bulled=14580679; DOI=10.1016/j.bbaexp.2003.08.010;
Matheus L., Blair G.B.;
"Identification and characterisation of a cDNA encoding a 17-kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAINSEPRAGE-DEWIEY;
Matheus L.M., Blair G.E.;
Submitted (CT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF439750; AAL84189.1; -; mRNA.
EMBL; AF439750; AAL84189.1; -; mRNA.
EMBL; AF439750; AML84189.1; -; mRNA.
InterPro; IPR00548; Myelin_BP.
FRINTS; PR00512; MYELINMBP.
ProDow; PD004542; MYELINMBP.
PROSITE; PS00569; MYELIN MBP; 1.
SEQUENCE 158 AA; 17240 MW; 3255580242ECC3E1 CRC64;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR536534; CAG38771.1; -; mRNA.
GO; GO:019911; F:structural constituent of myelin sheath; IEA.
InterPro; IPR000548; Myelin BP.
Princh: PR01669; Myelin MBP; 1.
PRINTS; PR00212; MYELINMBP.
Probom: PD004542; MYELINMBP; 1.
SEQUENCE 160 AA; 17347 MM; 0107AAD6053CDB76 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoform of rat myelin basic protein.";
Biochim. Biophys. Acta 1630:47-53(2003)
                                                                                       Created)
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                                                                               01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
Myelin basis ......
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QEFIO4;
QBR4K6_RAT PRELIMINARY;
Q8R4K6;
                                                                                                                                                                                                                                                                                                                                                                                           Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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MEDLINE-76025020; PubMed-51849;

The Contribution of phosphorylation and loss of COOH-terminal
The contribution of the COOH of the most abundant protein component of the myelin membrane in the COOH as a role in both the formation and stabilization of this compact multilayer arrangement of bilayers.

Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).

The SUBGNIT: Homodimer (By similarity).

SUBGNIT: Homodimer (By similarity).

The SUBGNIT: Homodimer (By similarity).
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Shapira R., McKneally S.S., Chou F., Kibler R.F.;
Encephalitogenic fragment of myelin basic protein. Amino acid
"Encephalicogenic fragment of guinea pig, monkey, and human fragments.";
J. Biol. Chem. 246:4630-4640(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nervous system.

The state of charge isomers; C1 (the most cationic, least modified, and most abundant form), C2, C3, C4 and C5 (the least cationic form); are produced as a result of optional posttranslational modifications such as phosphory/lation of serine or threonine residues, deamidation of glutamine or apparagine residues, citrullination and methylation of arginine residues. C1 and C2 are unphosphorylated, C3 and C4 are monophosphorylated and C5 is phosphorylated at two positions.

SIMILARITY: Belongs to the myelin basic protein family.
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTION SEQUENCE OF '-156.
STRAIN-HARTIEY; IISSUE-SPINI CORd;
Kim G., Tanuma N., Matsumoto Y.;
"DNA vaccination using Guinea pig myelln basic protein coding region
                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
                                                       ö
        100.0%; Score 94; DB 2; Length 160; 100.0%; Pred. No. 2.3e-07; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deibler G.E., Martenson R.E., Krutzsch H.C., Kies M.W.; "Sequence of guinea pig myelin basic protein."; J. Neurochem. 43:100-105(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in experimental autoimmune encephalomyelitis.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                       (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                167 AA
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MEDLINE=84215086; Pubmed=6202840;
                                                                                                                         84 ENPVVHFFKNIVTPRTP 100
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                                                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig)
                                                                                                ENPVVHFFKNIVTPRTP
                                                                                                                                                                                                                                                                                                                                                     Myelin basic protein (MBP)
           Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                  STANDARD;
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01-MAY-1992 (
10-MAY-2005 (
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                           Gaps
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Submitted (JUV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CRS41919; CAG4617.1; -; mRNA.
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Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger Spool G., Han M., Wiemann S.;

Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR860121; CAH92266.1; -; mRNA.

GO; GO:0019911; F:structural constituent of myelin sheath; IEA InterPro; IFR00548; Myelin BP.

Ffam; PF01669; Myelin MBP; I.

PRINTS; PR00212; MYELINMBP.
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Pred. No. 2.3e-07;
                   Length 160;
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160 AA; 17317 MW; 1A0601CCB257D9C6 CRC64;
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Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 2.3e-07;
ive 0; Mismatches 0;
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PROSITE; PS00569; MYELIN MBP; 1.
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Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSR7J4_PONPY PRELIMINARY;
QSR7J4;
                                                                                                                                                                                                                                                    QEFH37_HUMAN PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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SEQUENCE 16
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Lagomorpha, Leporidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Myelin basic protein (MBP) (Myelin Al protein) (Myelin Pl protein)
                                                                                                                                                               Phosphoserine (By similarity).
Phosphoserine (By similarity).
Citrulline (By similarity).
Citrulline (By similarity).
Phosphoserine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Deamidated glutamine (partial) (By similarity).
                                                                     Prodom; PD004542; Myelin BP; 1.
PROSITE; PS00569; MYELIN MBP; 1.
Acetylation; Autoimmune encephalomyelitis; Citrullination;
Direct protein sequencing; Methylation; Myelin; Phosphorylation;
Structural protein.
                                                                                                                                                                                                                                                             Phosphoserine (By similarity).
Citrulline (By similarity).
Deamidated glutamine (partial) (By
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                                                                                                                              encephalomyelitis (EAE) 1.
Induces experimental autoimmune
encephalomyelitis (EAE) 2.
                                                                                                                        Induces experimental autoimmune
                                                                                                                                                                                                                                                                                                          Phosphoserine (By similarity). Phosphoserine (By similarity).
                                                                                                                                                                                                                                             Symmetric dimethylarginine (By similarity).
                                                                                                                                                                                                                                                                                                                                                      Length 167;
                                                                                                                                                                                                                                                                                                                            Citrulline (By similarity).
866D31F1E5ACFEA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                          similarity).
Citrulline (By similarity)
                                                                                                                                                                                                                                                                                                                                                    Score 94; DB 1; L Pred. No. 2.4e-07; 0; Mismatches 0;
                                                                                                                                                           N-acetylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Biochem. Biophys. 153:590-598(1972)
               EMBL; AF074337; AAC26130.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Sciatic nerve;
MEDLINE=73190037; PubMed=4662101;
                                  HSSP; PO2686; 1QCL.
INTERPRO; IRRO00548; Myelin BP.
ANTHER; PTHR11429; Myelin BP; 1.
PFam; PF01669; Myelin MBP; 1.
PRINTS; PR00212; MYELINMBP.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                        PIR; A37246; A37246.
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162
167
167 AA;
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MBP_RABIT
ID _ MBP_RABIT
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SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                             myelin basic protein.";
J. Biol. Chem. 258:330-937(1983).

-! FUNCTION: Is, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splication of this compact multilayer arrangement of bilayers. Each splic variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).

-! SUBUNIT: Homodimer (By similarity).

-! SUBCELLULAR LOCATION: Cytoplasmic side of myelin.

-! TISSUE SPECIFICITY: Found in both the central and the peripheral
                                                   human fragments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as a result of optional posttranslatonial modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system.
PTM: As in other animals, several charge isomers may be produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                    Martenson R.E., Law M.J., Deibler G.E.; "Identification of multiple in vivo phosphorylation of multiple in vivo phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Omega-N-methylarginine (alternate).
Symmetric dimethylarginine (alternate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct protein sequencing, Methylation, Myelin, Phosphorylation, Structural protein.
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Shapira R., McKneally S.S., Chou F., Kibler R.F.;
"Encephalitogenic fragment of myelin basic protein. Amino acid
sequence of bovine, rabbit, guinea pig, monkey, and human fragm
J. Biol. Chem. 246:4630-4640(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deamidated glutamine (partial) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Induces experimental autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: The N-terminus is blocked.
SIMILARITY: Belongs to the myelin basic protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphoserine (By similarity). Citrulline (By similarity). Citrulline (By similarity).
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Citrulline (By similarity).
Phosphoserine (By similarity)
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PROSITE; PS00569; MYELIN MBP; 1.
Acetylation; Autoimmune encephalomyelitis; Citrullination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encephalomyelitis (EAE).
N-acetylalanine (Probable).
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Citrulline (By similarity).
S -> G (in Ref. 2).
EC3C97ACD2C08EA6 CRC64;
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                                                                                                                   PHÓSPHORYLATION.
MEDLINE=83108902; PubMed=6185481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02686; 1QCL.
INterPro; IPR000548; Myelin BP.
ANTHER; PTHR11429; Myelin BP; 1.
Pfam; PF01669; Myelin MBP; 1.
PRINTS; PR00212; MYELINMBP.
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18217 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of arginine residues.
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Matches 17; Conserv
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Shapira R., McKneally S.S., Chou P.C.-H., Kibler R.F.; "Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments."; J. Biol. Chem. 246:4630-4640(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-71153946; PubMed-4994464; Broseloff S.W., Bylaz E.H.; Broseloff S.W., Bylaz E.H.; "Localization of methylated arginine in the Al protein from myelin."; Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE REVISION.
MEDLINE:AFGO70688; PubMed=4129204;
MEDLINE:AFGO70688; PubMed=4129204;
Broatoff S.W., Reuter W., Hichens M., Eylar E.H.;
"Specific cleavage of the Al protein from myelin with cathepsin D.";
J. Biol. Chem. 249:559-567(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 30-42; 74-89 AND 114-129.
MEDLINE=96107211; PubMed=8530487; DOI=10.1074/jbc.270.51.30551;
Prasad K., Barouch W., Martin B.M., Greene L.E., Elsenberg E.;
"Purification of a new clathrin assembly protein from bovine brain coated vestcles and its identification as myelin basic protein.";
                                                                                                                                                                           MBP_BOVIN STANDARD; PRT; 169 AA.
P02667; Q9BGM8; Q9TS63; Q9TSA6;
P1-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa microtubule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         류
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bylar B.H., Brostoff S.W., Hashim G., Caccam J., Burnett P., "Basic Al protein of the myelin membrane. The complete amino acid
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pirollet F., Derancourt J., Haiech J., Job D., Margolis R.L., "Ca(2+)-calmodulin regulated effectors of microtubule stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION MEDLINE=70178977; PubMed=5442707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE OF 38-58 AND 119-141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.";
J. Biol. Chem. 246:5770-5784(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE.
MEDLINE=72007306; PubMed=5096093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 31:8849-8855(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                  Pecora; Bovidae; Bovinae; Bos.
                       ENPVWHEFKNIVTPRTP 17
                                              NUCLEOTIDE SEQUENCE OF 4-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN SEQUENCE OF 43-87
                                                                                                                                                                                                                                                                                                               stabilizing protein).
Name=MBP;
                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
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use as long as its content is in no way modified and this statement is not
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Biochemistry 19:1826-1831(1980).

Biochemistry 19:1826-1831(1980).

FUNCTION: Is, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bliayers. Bach splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).

-I SUBUNIT: Homodimer; self-associates in the presence of lysolipid.
-I SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
-I TISSUE SPECIFICITY: Found in both the central and the peripheral
                                                                                                                                                                                                                                                                 Erickson A.V., Payne D.M., Martino P.A., Rossomando A.J., Shabanowitz J., Weber M.J., Hunt D.F., Sturgill T.W.; "Identification by mass spectrometry of threonine 97 in bovine myelin basic protein as a specific phosphorylation site for mitogen-activated protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Sedimentation analysis of the self-association of bovine myelin basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99153125; PubMed-9485392; DOI=10.1021/bi972347t;
Zand R., Li M.X., Jin X., Lubman D.;
"Determination of the sites of posttranslational modifications in the charge isomers of bovine myelin basic protein by capillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nervous system.

PTM: At least 6 charge isomers; C1 (the most cationic and least modified form), C2, C3, C4, C5 and C6 (the least cationic form); are produced as a result of optional posttranslatonial modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.

SIMILARITY: Belongs to the myelin basic protein family.
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Induces experimental autoimmune encephalomyelitis (EAE) 2.
N-acetylalanine.
                                                                                                                                                                                                                      PROTEIN SEQUENCE OF 97-104, AND PHOSPHORYLATION SITE THR-97 MEDLINE=91060584; PubMed=1700979;
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                                                                                       Chou F.C.-H., Chou C.-H.J., Shapira R., Kibler R.F.; "Basis of microheterogeneity of myelin basic protein."; J. Biol. Chem. 251:2671-2679(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 265:19728-19735(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                electrophoresis-mass spectroscopy.";
Biochemistry 37:2441-2449(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POST-TRANSLATIONAL MODIFICATIONS.
[9]
POST-TRANSLATIONAL MODIFICATIONS.
MEDLINE=76167591; PubMed=57115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4SSP; P02686; 1QCL.
InterPro; IPR000548; Myelin BP.
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Pfam; PF01669; Myelin_MBP; 1.
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SEQUENCE
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-i- FUNCTION: Is, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).

-i- SUBCELDUAR LOCATION: Cytoplasmic side of myelin.

-i- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslatonial modifications, such as phosphorylation of serine or threonine residues, deamidation of serine or threonine residues, deamidation of serine or threoline residues, details on methylation of serine or threoline residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=76009821; PubMed=51459; DOI=10.1016/0024-3205(75)90506-8; Westall F.C., Thompson M., Kalter S.S.; "The proposed sequence of the encephalitogenic protein from chimpanzee
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                       Omega-N-methylarginine (alternate).
Symmetric dimethylarginine (alternate).
Phosphoserine (By similarity).
Citrulline (By similarity).
Deamdated glutamine (in form C2).
Citrulline (By similarity).
Phosphoserine (in C4 and C6).
Phosphoserine (in C3, C5 and C6).
                                                                                                                                                                                                                                                          Gaps
 Citrulline (By similarity).
Citrulline (By similarity).
Phosphoserine (in C4, C5 and C6).
Phosphoserine (By similarity).
Phosphothreonine (by WAPK) (in C3, C4, and C6).
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                                                                            Deamidated glutamine (in form C5)
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                                                                                                                                                                                                                                 Score 94; DB 1; Length 169;
Pred. No. 2.4e-07;
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10-MAY-2005 (Rel. 47, Last annotation update)
Myelin basic protein (MBP).
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InterPro; IPR000548; Myelin BP.
PANTHER; PTHR11429; Myelin BP; 1.
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                                                                                                                                                                                                                                 100.08;
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Preliminary protein sequence.
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Guery Match
Best Local Similarity 100.00
Conservative
Conservative
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169 AA;
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MBP_PANTR
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Kira J.-1., Deibler G.E., Krutzsch H.C., Martenson R.E.;
J. Neurochem. 44:1653-165(1985).

-!- FUNCTION: 18, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).
-!- SUBGNIT: Homodimer (By similarity).
-!- SUBGLIGILAR LOCATION: Cytoplasmic side of myelin.
-!- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslatonial modifications, such as
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RELUKTS; PRO0212; MYELIMED.

R PRODOM; PRO0542; MYELIMED.

R PRODOM; PRO0569; MYELIMED.

R PROSTE; PS00569; MYELIMED.

W Acetylation, Autoimmune encephalomyelitis; Citrullination;

M Direct protein sequencing; Methylation; Myelin; Phosphorylation;

M Direct protein.

N-acetylalanine.

N-acetylalanity).

N-acetylalanine.

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Citrulline (By similarity).
Citrulline (By similarity).
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Phosphoserine (By similarity)
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MEDLINE=B8056964; PubMed=2578056;
Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;
"Amin acid sequence of porcine myelin basic protein.";
J. Neurochem. 44:134-142(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
Omega-N-methylated arginine
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Citrulline (By similarity)
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E9FED59DE6933293 CRC64;
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30-MAY-2000 (Rel. 39, Last seqn
13-SEP-2005 (Rel. 48, Last anno
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les 17; Conservative
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Matches
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     SARRARARA
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                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                           R HSSP, P02666, 10CL.

R InterPro; IPRO00548; Myelin BP.

R PANTHER; PTR11429; Myelin BP.

R PANTHER; PTR11429; Myelin BP; 1.

R PRINTS; PR002612; MYELIN MBP; 1.

R PRODOM; P0004542; MYELIN MBP; 1.

R PROSTIE; PS00569; MYELIN MBP; 1.

R PROSTIE; PS00569; MYELIN MBP; 1.

R Myelin; Phosphorylation; Direct protein sequencing; Methylation; Myelin; Phosphorylation; Structural protein.

Myelin; Phosphorylation; Structural protein.

Myelin; Phosphorylation; Structural protein.

Myelin; Phosphorylation; Citrulline (By similarity).

T MOD_RES 12 25 Citrulline (By similarity).

T MOD_RES 55 Phosphoserine (By similarity).

T MOD_RES 55 Phosphoserine (By similarity).

T MOD_RES 70 70 Phosphoserine (By similarity).

T MOD_RES 98 98 Phosphothreonine (By similarity).

T MOD_RES 103 103 Boenmidated glutamine (partial) (By similarity).
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Nome-DKFZGF59C0215; Synonyms-DKFZGF459P2220;
Pongo pygmaeus (Orangutan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Symmetric dimethylarginine (alternate).
Phosphoserine (By similarity).
Deamidated glutamine (partial) (By
phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.
SIMILARITY: Belongs to the myelin basic protein family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphoserine (By similarity).
Phosphoserine (By similarity).
Citrulline (By similarity).
Citrulline (By similarity).
Phosphoserine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Deamidated glutamine (partial) (By similarity).
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The German cDNA Consortium;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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NUCLECTIDE SEQUENCE.

A Min J.G., Nonneman D., Vallet J.L., Rohrer G.A., Christenson R.K.; Chromosome 1.";

chromosome 1.";

L Anim. Genet. 36:163-164 (2005).

E REMBL; AY603684; AA728318.1; -; MRNA.

R CO, GO:0019911; F:structural constituent of myelin sheath; IEA.

R InterPro; IPR000548; Myelin BP.

R Pfam; PR01659; Myelin MBP; 1.

R PROSTITE; PS00569; MYELINMBP.

R PROSTITE; PS00569; MYELINMBP.

R PROSTITE; PS00569; MYELINMBP.

R PROSTITE; PS00569; MYELIN MBP; 1.

R PROSTITE; PS00569; MYELIN MBP; 1.

R PROSTITE; PS00569; MYELIN MBP; 1.
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Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR860682; CA492798.1; -; mRNA.

GO; GO:0019911; F:structural constituent of myelin sheath; IEA.

InterPro; IPR000548; Myelin BP.

Pfam; PR01612; Myelin BP; 1.

PRODM; PR01612; MYELIN BP; 1.

PRODM; PR004542; Myelin BP; 1.

PROSM:F; PS00569; MYELIN BP; 1.

Hypothetical protein.

ENGLIS, PS00569; MYELIN BP; 1.

SEQUENCE 171 AA; 18565 MW; F8B56E03D6305540 CRC64;
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100.0%; Pred. No. 2.5e-07;
ive 0; Mismatches 0; Indels
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Last annotation update)
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Best Local Similarity 100.
Matches 17; Conservative
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QGJZR3;
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Best Local Similarity
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

February 22, 2006, 21:31:15; Search time 1.7323 Seconds (without alignments) 944.229 Million cell updates/sec Run on:

US-10-000-439-13 94 1 ENPVVHFFKNIVTPRTP 17 score: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Sequence:

Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri: piri: piri: PIR 80:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

hypothetical prote	hypothetical prote	cytosine/guanine d	probable peptide m	probable ribonucle	hypothetical prote	ATM-like protein [	hypothetical prote	protein F41H10.2 (	glutamate racemase	hypothetical prote	hypothetical prote	C4-dicarboxylate-b	conserved hypothet	conserved hypothet	o-succinylbenzoate
T27005	AD2530	D96934	T50177	H72510	T51040	C85426	T05501	F88690	B81262	F86897	T15311	S18578	F89944	H70302	AB0308
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892	192	428	431	983	1162	2089	3738	164	250	270	323	333	337	431	471
43.6	42.6	42.6	42.6	42.6	42.6	42.6	42.6	41.5	41.5	41.5	41.5	41.5	41.5	41.5	41.5
41	40	40	40	40	40	40	40	39	39	33	39	39	33	39	39
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

myelin basic protein S - rat

N;Alternate names: small myelin basic protein

N;Alternate names: small myelin basic protein

N;Alternate names: small myelin basic protein

C;Species: 24-Apr-1984 #sequence revision 08-Feb-1996 #text\_change 09-Jul-2004

C;Accession: B24351; A90275; A94243; A21062; A03142

C;Accession: B24351; A90275; A94243; A21062; A03142

Biol. Chem. Hoppe-Seyler 367, 825-834, 1986

A;Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the A;Reference number: A24351; MUID:87026249; PMID:2429678

A;Accession: B24351

A;Molecule type: mRNA A;Residues: 1-128 eSCH3-A;Cross-references: UNIPROT:P02688; UNIPARC:UPI0000163B8F; EMBL:M25889; NID:g205321; PI: R;Dunkley, P.R.; Carnegie, P.R. B;Dunkley, P.R.; Carnegie, P.R. B;Ochem. J. 141, 243-255, 1974 A;Title: Amino acid sequence of the smaller basic protein from rat brain myelin. A;Reference number: A90275; MUID:75127359; PMID:4141893

A,Accession: A90275
A,Molecule type: protein
A,Molecule type: protein
A,Residues: 2-128 <br/>
A,Cross-references: UNIPARC:UPI000002ADB4
A,Cross-references: UNIPARC:UPI000002ADB4
A,Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in th
A,Note: rats have two myelin basic proteins; the smaller one, shown above, is missing 40
R;McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McKneally, S.; Shapira, R.
A;Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogen'
A;Reference number: A94243; MUID:73180720; PMID:4122324 A; Accession: A94243

A; Molecule type: protein
A; Molecule type: protein
A; Residues: 46-86 < MCF.
A; Cross-references: UNIPARC: UP100001740CC
A; Cross-references: UNIPARC: UP100001740CC
A; Note: the sequence reported for this encephalitogenic peptide differs from that shown
R; Roach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.B.
A; Polyonof, 1993
A; Title: Characterization of cloned cDNA representing rat myelin basic protein: absence
A; Reference number: A21062; MUID: 84026484; PMID: 6194889

A; Molecule type: mRNA

A;Readdues: 1.124, TI, 126-128 <ROA>
A;Cross-references: UNIPARC:UP1000002E780
A;Cross-references: UNIPARC:UP1000002E780
A;Experimental source: strain Sprague-Dawley
C;Superfamily: myelin basic protein
C;Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalom;
P;2-128/Product: myelin basic protein S #status experimental <AMI>
F;2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #stat:
F;2/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

ö Gaps ö Query Match 100.0%; Score 94; DB 1; Length 128; Best Local Similarity 100.0%; Pred. No. 9.6e-09; Matches 17; Conservative 0; Mismatches 0; Indels

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A;Cross-references: UNIPARC:UP100001740BD
R;Okazaki, K.; Obata, N.H.; Inove, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
Ajtile: S100-beta is a target protein of neurocalcin delta, an abundant isoform in gli
A;Reference number: S54343; MUID:95194333; PMID:7887910
                                                                                                                                                                                 A; Molecule type: protein
A; Molecule type: protein
A; Reaidues: 74-75, 'HG, '78-22,'D', '84-88;105,'X',107-108,'X',110-114,'X',116-119 <OKA>
A; Reaidues: 74-75,'HG,'78-22,'D', '84-88;105,'X',107-108,'X',110-114,'X',116-119 <OKA>
A; Crachances: UNIPARC:UP100001740BE; UNIPARC:UP100001740BE
R; Takamatau, K.; Tatemoto, K.
Neurochem. Res. 17, 239-246, 1392
Neurochem. Res. 17, 239-246, 1392
A; Title: Isolation and characterization of two novel peptide amides originating from my: A; Reference number: A61641; MUID:92319189; PMID:1377792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPARC: UPI00001740C0
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J. Biol. Chem. 246, 4630-4640, 1971
J. Biol. Chem. 246, 4630-4640, 1971
J. Biol. Chem. 246, 4630-4640, 1971
A;Fille: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin A;Reference number: A92087
A;Accession: C92087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nictrate names: myelin Al protein
Nicontains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16)
Cispecies: Bos primigentus taurus (cattle)
Cispecies: Bos primigentus taurus (cattle)
Cispecies: Bos primigentus taurus (laber-1981 #text_change 09-Jul-2004
Cistcession: A92089; A92160; A92087; S54343; A61641; B61641; A03140
R;Eylar, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P.
J. Blol, Chem. 246, 5770-5784, 1911
A;Title: Basic Al protein of the myelin membrane. The complete amino acid sequence. A;Reference number: A92089; MUID:72007306; PMID:5096093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                            myelin basic protein - guinea pig
NyAlternate names: myelin Al protein
Cispecies: Cavia myelin Al protein
Cispecies: Cavia porcellus (guinea pig)
Cipate: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
Cispeciesion: A37-246; C92087; A03140
Cispeciesion: A37-246; C92087; A03140
J. Neurochem. 43, 100-105, 1984
A;Thle: Sequence of guinea pig myelin basic protein.
A;Reference number: A37-246; MUID:84215086; PMID:6202840
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A; Residues: 1, %, 2-169 «EXL»
A; Cross-references: UNIPROT: P02687; UNIPARC: UPI0000148533
R; Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.
J. Biol. Chem. 249, 559-567, 1974
A; Title: Specific cleavage of the Al protein from myelin with cathepsin l
A; Reference number: A92160; MUID: 74070688; PMID: 4129204
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A,Molecule type: protein
A,Residus: 1-17 <DEI:
A,Crose-references: UNIPROT: P25188; UNIPARC: UPI000012ED39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94; DB 2; I
Pred. No. 1.3e-08;
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C;Superfamily: myelin basic protein
C;Keywords: myelin
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                                                                                                 ENPVVHFFKNIVTPRTP 97
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Best Local Similarity 100.0
----hes 17; Conservative
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A; Molecule type: protein
A; Residues: 1-16 - CTA2.
A; Residues: 1-16 - CTA2.
A; Cross-references: UNIPARC:UPI00001740C0
A; Residues: 1-16 - CTA2.
A; Cross-references: UNIPARC:UPI00001740C0
A; Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymat R; Brostoff, S.; Eylar, E.H.
B; Brostoff, S.; Eylar, E.H.
A; Contents: annotation of methylated arginine in the Al protein from myelin.
A; Reference number: A3377; MUID:71153946; PMID:4994464
A; Contents: annotation of methylarginine and dimethylarginine
A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine
A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine
A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine
A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine
A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine
A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine
A; Note: Arg-106 is modified to monomethylarginine and dimethylarginine
A; Note: Arg-106 is modified to monomethylarginine
A; Note: Arg-106 is modified to monomet
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A; Residues: 1-171 A; Residues: 1-171 A; Residues: 1-171 C; Comment: This protein may function in maintaining the proper structure of myelin. C; Comment: This protein may function in maintaining the proper structure of myelin. C; Superfamily: myelin basic protein
C; Superfamily: myelin basic protein
C; Meyvords: blocked amino end; methylated amino acid; myelin; structural protein
C; JModified site: blocked amino end (Ala) (probably acetylated) #status experimental
F;107/Modified site: omega-N-methylarginine or omega-N, omega-N, -dimethylarginine (Arg)
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C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A03139
R;Westerll, FC.7; Thompson, M.; Kalter, S.S.
Life Sci. 17, 219-223, 1975
A;Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.
A;Reference number: A03139; MUID:76009821; PMID:51459
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N;Alternate names: MBP
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A;Accession: A94106
A;Molecule type: mRNA
A;Residues: 1-59,86-197 <KAM>
A;Cross-references: UNIPARC:UP1000002ADA6; GB:M13577; NID:g187408; PIDN:AAA59562.1; PID
A;Accession: B94106
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A; Residues: 2-59,86-197 < PRO>
A; Residues: 2-59,86-197 < PRO>
A; Residues: 2-59,86-197 < PRO>
A; A; Cross=references: University  
A; Cross=references: Drain
B; Scoble, H.A.; Whitaker, J.N.; Biemann, K.
A; Neurochem. 47, 614-616, 1986
A; Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44 an A; Reference number: A60862; MUID:86280476; PMID:2426402
A; Accession: A60862
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A; Residues: 2-45;117-197 <SCO>
A; Cross-references: UNIPARC:UP100001740B8; UNIPARC:UP100001740B9
A; Note: evidence for acetylated amino end
R; Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.
A; Biol. Chem. 259, 5028-5031, 1984
A; Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined in A; Reference number: A61420; MUID:84185608; PMID:6201481
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A; Residues: 46-59,86-116 <GIB>
A; Residues: 46-59,86-116 <GIB>
A; Residues: 46-59,86-116 <GIB>
A; Cross-references: UNIPARC:UP100001740BA
R; Wood, D.D.; Moscarello, M.A.
J. Biol. Chem. 264, 5121-5127, 1989
A; Title: The isolation, characterization, and lipid-aggregating properties of a citrull:
A; Reference number: A33273; MUID:89174797; PMID:2466844
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A;Note: form C-8; residues designated 'X' were determined as citrulline
R;Baldwin, G.S.; Carnegie P.R.
Biochem. J. 123, 69-74, 1971
A;Title: Isolation and partial characterization of methylated arginines from the enceph-A;Reference number: A90257; MUID:72066401; PMID:5128665
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A;Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approx
B;Lennon, V.A.; Wilka, A.V.; Carnegie, P.R.
J. Immunol. 105, 1223-1230, 1970
A;Reference number: A92806; MUID:71088405; PMID:4099924
A;Contents: annotation
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Afritle: Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a new form of
A;Reference number: 154219; MUID:90152679; PMID:1689270
A;Accession: 154219
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R;Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prusiner, S.B.
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A;Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.
A;Reference number: A90256; MUID:72066400; PMID:4108501
A;Accession: A90256
A,Title: Identification of three forms of human myelin basic protein by cDNA cloning.
A,Reference number: A94106, MUID:86259714, PMID:2425357
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPARC:UP1000002ADA4
A;Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form A;Note: a 17.2K splice form is also described
A;Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form;
R;Carnegie, P.R.
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Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993
A;Title: Leukocyte gelatinase B cleavage releases encep)
A;Reference number: JH0802; MUID:93282820; PMID:7685161
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A;Residues: 2-59,86-197 <CAR>
A;Cross-references: UNIPARC:UP10000113626
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A; Residues: 1-197 < KA2>
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A, ACCESSION: A61640
A; Molecule type: protein
A, Residues: 1-17 < KTR>
A; Residues: 1-17 < KTR>
A; Residues: UPID: B81558; UNIPARC: UPI000012ED3E
A; Note: some peptides were ordered by homology
A; Takamatsu, K.; Tatemoto, K.
B; Dakamatsu, K.; Tatemoto, K.
B; Dakation and characterization of a novel peptide amide from porcine brain.
A; Reference number: A36245; MUD: 91058553; PMID: 1700904
A; Recession: A36245; MUD: 1800001
A; Recession: A3624
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C'Accession: Sloka2; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219; I56
R;Streicher, R.; Stoffel, W
Biol. Chem. Hoppe-Seyler 370, 503-510, 1989
A;Title: The organization of the human myelin basic protein gene. Comparison with the mc
A;Reference number: S10482; MUID:89302693; PMID:2472816
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A;Residues: 1-197 <STR.
A;Residues: 1-197 <STR.
A;Cross-references: UNIPROT:P02686; UNIPARC:UPI000002ADA4; EMBL:X17286; NID:G34490; PIDN
R;Kamholz, J.; De Ferra, F.; Puckett, C.; Lazzarini, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986
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N;Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein pred
.5K splice form
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NyAlternate names: myelin Al protein
NyContains: myelin basic protein amide 14
NyContains: myelin basic protein amide 14
C;Species: Sus serorfa domestica (domestic pig)
C;Species: 19-Apr-1996 #sequence_revision 26-Apr-1996 #text_change 09-Jul-2004
C;Accession: A61640; A36245
R;Kira, J.; Deibler, G.E; Krutzsch, H.C.; Martenson, R.E.
A;Neurochem, 44, 134-142, 1985
A;Title: Amino acid sequence of porcine myelin basic protein.
A;Reference number: A61640; MUID:85056964; PMID:2578056
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Pred. No. 1.3e-08;
Mismatches 0; Indels
                                                     Length 171;
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100.0%; Score 94; DB 1; I
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0;
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100.0%; Score 94; DB
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 17; Conservative 0; Mismatches
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A;Reference number: A45421; MUID:93186801; PMID:7680345
A;Accession: A45421
A;Molecule type: mRNA
A;Residues: 1-190;217-756;316-328 <CAMI>
A;Cross-rences: UNIPROT:P04370; UNIPARC:UPI00001740C3; UNIPARC:UPI00001740C4; UNIPARA;Experimental source: clone J37
A;Rote: sequence extracted from NCBI backbone (NCBIN:126696) and modified
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R; de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molineaux, S.; Lazzarin:
Cell 43, 721-727, 1985
A; Title: Alternative splicing accounts for the four forms of myelin basic protein.
A; Reference number: A90875; MUD:86079555; PMID:2416470
A; Reference number: A90875
A; Residues: 134-328 ADE>
A; Residues: 134-328 ADE>
A; Residues: 134-328 ADE>
A; Residues: 134-328 ADE>
A; Cross-references: UNIPARC:UPI00002ADA9; GB:L00404; GB:M11669; NID:g199060; PIDN:AAA3
A; Experimental source: 21.5K
A; Takahashi, N.; Roach, A.; Teplow, D.B.; Prusiner, S.B.; Hood, L.
Cell 42, 139-148, 1985
A; Riftle: Cloning and characterization of the myelin basic protein gene from mouse: one a shandard and characterization of the myelin basic protein gene from mouse: one a shandard and characterization of the myelin basic protein gene from mouse: one a shandard and characterization of the myelin basic protein gene from mouse: one a shandard and characterization of the myelin basic protein gene from mouse: one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene from mouse one a shandard and characterization of the myelin basic protein gene and the 
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A;Residues: 134-274;316-328 <NEM1>
A;Cross-references: UNIPARC:UPI00001740C5, UNIPARC:UPI00001740C8; GB:M15060; NID:g19904
A;Experimental source: clone M722; splice form 17.22K
A;Accession: B26591
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A; Residues: 134-190;217-263;275-328 «NEW2>
A; Cross-references: UNIPARC:UPI00001140C6; UNIPARC:UPI00001740C9; UNIPARC:UPI00001740CA|
A; Experimental source: clone M78; splice form 17.24K
B; Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V.W|
D. Neurochem. 54, 2032-2041, 1990
A; Title: Expression of a novel transcript of the myelin basic protein gene.
A; Reference number: A60920; MUID:90250449; PMID:1692584
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A;Residues: 1-191, 'SSEP' <CAM2>
A;Cross-references: UNIPARC:UP10000004029; GB:L07508; NID:g193586; PIDN:AAA37721.1;
A;Experimental source: clone BG21
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R;Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A. Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984
A;Title: Characterization of mouse myelin basic protein messenger RNAs with a A;Reference number: I58996; MUID:84119431; PMID:6198644
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A; Residues: 134-190; 217-274; 316-328 < KIT>
A; Residues: 134-190; 217-274; 316-328 < KIT>
A; Crosas references: UNIPARC: UD100001740C5; UNIPARC: UP100001740C6; UNIPARC: UP100001740C5; UNIPARC: UP100001740C6; UNIPARC: UP100001740C6; UNIPARC: UP100001740C6; UNIPARC: UP100001740C6; UNIPARCIMENTAL Sequence: M4; September: 59, 2318-2323, 1992
A; Title: A novel transcript overlapping the myelin basic protein gene. A; Reference number: 148407; MUID: 93057537; PMID: 1279125
A; Accession: 148407
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-191,'SSEP' <GRI>
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A; Status: preliminary
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C, Superfamily: myelin basic protein
C, Superfamily: myelin basic protein
C, Keywords: acetylated amino end; alternative splicing; citrulline; experimental autoimm
E;2-132,144-197/Product: myelin basic protein, 21.5K splice form #status predicted «MAT2
F;2-132,144-197/Product: myelin basic protein, 18.5K splice form #status experimental «MAT
F;2-59,86-132,144-197/Product: myelin basic protein, 18.5K splice form #status predicted
F;2-Modified site: acetylated amino and (Ala) (in mature form) #status experimental
F;26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experiment
F;134/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg) (
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N;Alternate names: golli-mbp protein; MBP
N;Ontains: myelin basic protein;
C;Contais: myelin basic protein;
C;Species: Mus musculus (house mouse)
C;Date: 17-Mar-1987 #sequence revision 07-Oct-1994 #text change 09-Jul-2004
C;Accession: A45421; B45421; A90875; A90867; A26591; B26591; A60920; I48407; I58996; I54
R;Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Landry, J. Biol. Chem. 268, 4930-4938, 1993
A;Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene that e
                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: mRNA; Molecule type: molecule 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-reference: UNIPARC:UPI000002ADA4; GB:M30515; NID:g187412; PIDN:AAA59564.1; PID: R;Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.; Campagnoni, A.T. J. Neurosci. Res. 16, 227-238, 1986
J. Neurosci. Res. 16, 227-238, 1986
A;Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin A;Reference number: I56565; MUID:86308101; PMID:2427738
                                                                                                                                                                                                GB:M63599; NID:g187402; PIDN:AAA59560.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPARC:UP1000002ADA5; GB:M30516; NID:g187410; PIDN:AAA59563.1; PID
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A;Cross-references: UNIPARC:UP100001740BC
C;Comment: Four alternatively spliced forms of myelin basic protein have been observed,
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; Status: preliminary; translated from GB/EMBL/DDBJ; Status: preliminary; translated from GB/EMBL/DDBJ; Robled: 1979; RRB3>
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A;Ataus: preliminary; translated from GB/EMBL/DDBJ
A;Ataus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-132,144-197 <RE2>
A;Cross-references: UNIPARC:UPI000002ADA5; GB:M30510
A;Accession: I73634
A;Status: preliminary; translated from GB/EMBL/DDBJ
preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
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                                                                                                                                                                                                Cross-references: UNIPARC:UPI000016AD10;
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nes 17; Conservative
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Cispecies: Heterodontus francisci (horn shark)
Cispecies: L.-Eeb-1990 #sequence_revision 21-Feb-1990 #text_change 09-Jul-2004
Cispace: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 09-Jul-2004
Cispacession: B32999
Risaavedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, A; Saavedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, A;Title: The myelin proteins of the shark brain are similar to the myelin proteins of the A;Reference number: A32999; MUID:90040744; PMID:2478717
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A;Cross-references: UNIPROT:P20939; UNIPARC:UPI00001713F7; GB:X17664; NID:g63974; PIDN:C
C;Superfamily: myelin basic protein
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C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Cates: Methanococcus jannaschii
C;Catession: G64440
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1996
A,Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, V.A.; Miller Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschin A;Reference number: A64300; MUID:96337999; PMID:8688087
A,Accession: G64440
A,Accession: G4440
A,Accession: G4440
A,Accession: Janna A,Accession: Galler A, Galler
myelin basic protein - dusky shark (fragments)
C;Species: Carcharhinus obscurus (dusky shark)
C;Accession: A60215
R;Milne, T.J.; Atkins, A.R.; Warren, J.A.; Auton, W.P.; Smith, R.
J. Neurochem: S5, 956-955, 1990
A;Title: Shark myelin basic protein: amino acid sequence, secondary structure, and shittle: Abark myelin basic protein: amino acid sequence, secondary structure, and shittle: Abark myelin basic protein: A;Reference number: A60215; MUID:90347482; PMID:1696624
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A;Note: the source was designated as Carcharhinus obscurus (whaler shark)
C;Superfamily: myelin basic protein
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Pred. No. 0.0065;
6; Mismatches 2; Indels
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Pred. No. 0.13;
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C,Superfamily: hypothetical protein MJ1128
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52.9%;
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Best Local Similarity 53.37
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A60215
A;Molecule type: protein
A;Residues: 1-128 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: B32999
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Gene organization and transcription of duplicated MBP genes of myelin deficient A;Reference number: IS3256; MUID:88196094; PMID:2452084
A;Reference number: IS3256
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 217-229, MIM', 232-250 < CKA>
A;Residues: 217-229, MIM', 232-250 < CKAP
A;Residues: 217-220, MIM', 232-200, MIM', MIM', Structural protein
A;Residues: Golli-mbp; Mim', Mim', Structural protein
C;Reywords: alternative splicing; Myelin; splice form 11K-# status predicted AMP
F;134-130, 217-276, 316-328/Product: myelin basic protein, splice form 11K-# status predicted
F;134-190, 217-263, 275-328/Product: myelin basic protein, splice form 11K-# status predicted
F;134-190, 217-263, 275-328/Product: myelin basic protein, splice form 11K-# status predicted
F;134-190, 217-274, 316-328/Product: myelin basic protein, splice form 11K-# status predicted
F;134-190, 217-274, 316-328/Product: myelin basic protein, splice form 11K-# status predicted
F;134-190, 217-274, 316-328/Product: myelin basic protein, splice form 11K-# status predicted
                                                 A;Residues: 219-248 <ZEL>
A;Residues: 219-248 <ZEL>
A;Crose-references: UNIPARC:UPI000016CED2; GB:K00989; NID:g199037; PIDN:AAA39495.1; PID:
B;Miura, M.; Tamura, T.
Gene 75, 31-38, 1989
A;Title: The promoter elements of the mouse myelin basic protein gene function efficient
A;Reference number: 154033; MUID:89252919; PMID:2470651
A;Accession: 154033
A;Accession: 15
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(Species: Gallus gallus (chicken)
(Species: Gallus gallus (chicken)
(Space: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
(Space: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
(Spacession: 808335 #sequence_revision and heterogeneity of myelin basic protein transcript A; Reference number: 808535; MUID: 89358239; PMID: 2475444
A; Reference number: 808535
A; Residues: 1-174 < ZOP>
A; Residues: 1-174 < ZOP>
A; Residues: 1-174 < ZOP>
A; Copperfamily: myelin basic protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.6%; Score 87; DB 2; Length 174; 88.2%; Pred. No. 2.2e-07; ive 2; Mismatches 0; Indels
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 17; Conserv
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RESULT 8

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Gaps

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0; Indels

Length 14;

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C;Species: Pisaster ochraceus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S12904
R;Sanghera, J.S.; Abersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A;Title: Identification of the sites in myslin basic protein that are phosphorylated by A;Reference number: S12904; MUID:91032186; PMID:1699809
A;Accession: S12904
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <SAN>
A;Cross-references: UNIPROT:Q7M3M4; UNIPARC:UP1000017BF0C
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                        45.7%; Score 43; DB 2;
100.0%; Pred. No. 0.41;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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C;Species: Neurospora crassa
C;Date: 19 = Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: T46577
R;Baker, D.L.; Paietta, J.V.
R;Baker, D.L.; Paietta, J.V.
R;Baker, D.L.; Paietta, J.V.
A;Description: Molecular characterization of the arylsulfatase gene of Neurospora crassa
A;Reference number: Z23090
A;Accession: T46577
A;Cacession: T6577
A;Adeus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-639 cBAK>
A;Cross-references: UNIPROT:043113; UNIPARC:UPI000006B2E2; EMBL:U89492; PIDN:AAC02716.1
C;Genetics:
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A;Note: genes are expressed under conditions of sulfur limitation and are under coordins C;Superfamily: arylsulfatase, plant type
C;Keywords: sulfuric ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A57246
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-329 <KILI>
A;Cross-references: UNIPROT:P54097; UNIPARC:UPI0000136B89; GB:L38519; NID:g602439; PIDN:
                                                                                                                                                                                                                                                                                                                      C;Date: 10-Nov-1995 #Bequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C;Accession: A57246  
R;Killikck, R; Legan, P.K.; Malenczak, C.; Richardson, G.P. J. Cell Biol. 129, 535-547, 1995 A;Title: Molecular cloning of chick beta-tectorin, an extracellular matrix molecule of A;Reference number: A57246; MUID:95238547; PMID:7721949
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                                                                                                                                                                                                                                                                      beta-tectorin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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       Length 308;
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                                                       1; Indels
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S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
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Pred. No. 11;
4; Mismatches
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Pred. No. 23;
       Score 45; DB 2;
Pred. No. 6.7;
2; Mismatches
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     Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative 5
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Best Local Similarity 50.0%;
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91 KNPVYHFYNSIVS 103
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Best Local Similarity 53.5.
7, Conservative
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| HLFPDVIVPRTP 293
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A;Introns: 115/1; 518/3
C;Function:
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89965
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                     A;Accession: C89965
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <KUR>
A;Cross-references: UNIPROT:Q99T75; UNIPARC:UPI000013B193; GB:BA000018; PID:g13701588;
conserved hypothetical protein SA1613 [imported] - Staphylococcus aureus (strain N315)
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                                                                                                                                                                                                                          A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 3 Pred. No. 3.3; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental Bource: strain N315 C, Genetics: A, Gene: SA1613
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Myelin ba
Peptide r
Peptide a
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Human mye
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Myelin ba
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HLA bindi
HLA bindi
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                                                         February 22, 2006, 21:24:11; Search time 11.1572 Seconds (without alignments) 669.475 Million cell updates/sec
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Aac20308 |
Aac2359 |
Abp97941 |
Abr56063 (
Aac19672 |
Adw36476 |
Adw36476 |
Adw36476 |
Adw37704 |
Adw41115 |
Aar32295 SAar441113 |
Aar44113 |
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                              2443163
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                        2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                        - protein search, using sw model
                                                                                                                                                                                                                                                                  summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE26359
AAE23935
ABP97941
ABR56063
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ADE50773
ADW36476
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ADW33812
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Gapop 10.0 , Gapext 0.5
                                                                                                                     ENPVVHFFKNIVTPRTP 17
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36	, Q	0.00	19	9 0	AAR95366 AAD06366	Aar95366	Residues
27	0 4 4	100.0	19	N 61	AAR95358	Aar95358 Aar95358	Residues
28	94	100.0	19	~	AAW34183	Aaw34183	Bt-MBP (84
29	94	100.0	19	N	AAW34180	Aaw34180	Residues
30	94	100.0	19	~	AAW18021	Aaw18021	Human BPP
31	94	100.0	19	7	AAW44071	Aaw44071	Human mye
32	94	100.0	19	N	AAW73607	Aaw73607	Human mye
33	94	100.0	19	N	AAW73616	Aaw73616	Human mye
34	94	100.0	19	m	AAY58992	Aay58992	Myelin ba
35	94	100.0	19	m	AAY85560	Aay85560	Human MBP
36	94	100.0	19	m	AAY85550	Aay85550	Human MBP
37	94	100.0	19	m	AAY66532	Aay66532	Myelin ba
38	94	100.0	19	m	AAY66543	Aay66543	Myelin ba
39	94	100.0	19	ო	AAB12618	Aab12618	Human mye
40	94	100.0	19	m	AAB12613	Aab12613	Human mye
41	94	100.0	19	4	AAM99040	Aam99040	Vaccine r
42	94	100.0	19	4	AAB74440	Aab74440	Ovalbumin
43	94	100.0	19	4	AAG65171	Aag65171	Myelin ba
44	94	100.0	19	S	ABG31665	Abg31665	Myelin ba
45	9	0 00 1	0	r	00055WUV	000000000000000000000000000000000000000	LIN DANGE

# ALIGNMENTS

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Human; myelin basic protein; oligodendroglial cell; Th2 immune response; Th2-type cytokine; analogue; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crowe P;
                                                                                                                                                                                                                                                                                               Peptide derived from a human myelin basic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staehlin T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GES MBH
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW (
(NEUR-) NEUROCRINE BIOSCIENCES INC
                                                                        AAY69395 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US019033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00137759
                                                                                                                                                                                                                      19-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                 AAY69395;
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AAY69395
AAY
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WPI; 2000-224661/19

immune response Inducing a Th2 immune response and a persistent systemic immune respont to myelin basic protein, MBP, or a peptide analog of MBP for use in treating multiple sclerosis, by administering compositions comprising peptide analogs of MBP.

Example 10; Fig 8; 112pp; English.

The present sequence represents a peptide derived from human myelin basic protein. Myelin basic protein is found in the cytoplasm of human oligodendroglial cells. Peptide analogue derived from the present sequence are administered to a patient in need to induce a Th2 immune response (i.e. production of T cells producing one or more Th2-type cytokines) and/or a persistent systemic immune response to myelin basic protein. These peptide analogues are at least seven amino acids long, derived from residues 83-99 of human myelin basic protein and altered

Human mye Human mye Human MBP

Residues

Myelin ba

AAY66533 AAR32295

AAR85132 AAW05719

4AR44123

Sequence

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Gaps

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The present invention relates to a novel method for inducing Th2 immune responses to Myelin Basic Protein (MBP) or a peptide analogue of MBP in a patient. The method involves administering a composition comprising the MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for treating multiple sclerosis (MS). Sequences of the invention are also used as vaccines. The present sequence is a peptide related to human MBP
of the invention of peptide region 83-99 of Myelin basic protein (MBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducing Th2 immune responses to Myelin Basic Protein (MBP) by administering the MBP peptide analog CGP 77116, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The immune response, myelin basic protein, MBP; vaccine, MS; multiple sclerosis; antisclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 94; DB 5; 100.0%; Pred. No. 7e-09;
                                                                                 Score 94; DB 5;
Pred. No. 7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide related to myelin basic protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conlon P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multiple Sclerosis.
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                                                                                                       Local Similarity
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                                           Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1999;
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                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for selecting a tolerogenic peptide, comprising selecting a peptide which is capable of binding to a major histocompatibility complex (MHC) class I or II molecule without further processing. The peptides of the invention are useful for preventing a disease such as hypersensitivity disorder, and also for treating and/or preventing a disease in a subject. The method involves identifying an intigen for the disease, identifying an apitope (antigen processing independent epitope) for the antigen, and administering the apitope to the subject. The peptides of the invention are also useful for treating independent epitope) for the invention are also useful for treating curricaria, autoimmune diseases such as multiple sclerosis, altergoic thinitis, utricaria, autoimmune diseases under a multiple sclerosis, autoimmune thyroiditis, Grave's disease, systemic sclerosis, arcoidosis, autoimmune trejection. The peptides are also useful for modifying antiviral CD8+ responses in a tolerogenic fashion. This sequence represents an apitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dermacological, antiallergic, neuroprotective; antithyroid; antianaemic, vasotropic, antinflammatory; immunosuppressive; antidiabetic, class I; major histocompatibility complex; MHC; class II; autoimmune thyroiditis; hypersensitivity disorder; antigen; allergy; extrinsic asthma; utricaria; autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis; autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis; systemic sclerosis; polymyositis; diabetes; transplant rejection;
    positions 91, 95 or 97. The peptide treatment of multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myelin basic protein; apitope; antiasthmatic; tolerogenic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selecting tolerogenic peptide useful for treating autoimmune diseases e.g. multiple sclerosis, involves selecting peptide which binds major histocompatibility complex class I or II molecule without further
                                                                                                                                                     Gaps
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                                                                                                         Score 94; DB 3; Length 17; Pred. No. 7e-09;
                                                                                                                                                0; Indels
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                                                                                                                                                     Mismatches
      from the native sequence at least at analogs are especially useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mazza G,
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                                                                                                                                                                                                                                                                                                                                           AAO20308 standard; peptide; 17
                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                             Local Similario,
les 17; Conservative
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                                                                 Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiviral CD8+
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                                                                                                           Query Match
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Gaps

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Length 17; 0; Indels

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Immunoabsorption column, useful for treating multiple sclerosis, contains glycopeptides able to react with disease-specific autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                           containing conjugates comprising glycopeptides which are able to recognize antibodies implicated in multiple sclerosis. The column removes harmful antibodies selectively, leaving all other components of the serum unchanged. The column is used to treat multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                       ABP97937-44 represent glycopeptides of a formula given in the specification. The glycopeptides are used to produce columns of the invention. The specification describes immunoabsorption columns,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycopeptide #5 for diagnosis and treatment of multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel glycopeptides comprising a specific tetrapeptide, useful as diagnostic tools for identifying multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycopeptide; neuroprotective; autoantibody; multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 94; DB 6; Length 17; 100.0%; Pred. No. 7e-09; Live 0; Mismatches 0; Indels
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                                                                                                                                                                   Rovero P,
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                                                                                                                                                                   Chelli M,
                                                                                                                                                                                                                                                                                       Claim 4; Page 6; 13pp; English.
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                                                                25-JUL-2002; 2002WO-EP008274
                                                                                                25-JUL-2001; 2001IT-FI000144
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                                                                                                                                                                   Pinto F, Papini AM,
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les 17; Conserv
WO2003009887-A2.
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-2003
                                06-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papini AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR56063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                           novel peptide used in the treatment of autoimmune disease e.g. multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a peptide used in the treatment of autoimmune disease e.g. multiple sclerosis (MS). More particularly, it concerns a Teel receptor sequence found in some MS patients and methods for its detection. T cell receptors comprise alpha and beta chains, with beta chains comprising the following regions from N-terminus to C-terminus. Wbeta-Dbeta-Dbeta-Cheta. T cell receptors naturally vary in the Vbeta-Dbeta-Dbeta-Grean. The peptides of the invention are used for treating autoimmune disease e.g multiple sclerosis. The present sequence is a peptide analogue used in the exemplification of the invention
                                                                              Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Ubeta; Dbeta; immunosuppressive; T-cell receptor; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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Pred. No. 7e-09;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycopeptide; serum; immunoabsorption column; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residue"
                                              Peptide analogue used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a glycopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "OH attached"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "H attached"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 2; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP97941 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                    22-AUG-2000; 2000WO-US022988
                                                                                                                                                                                                                                                                     22-AUG-2000; 2000WO-US022988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ENPVOHFFKNIVTPRTP
              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-454317/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 AA;
                                                                                                                                                                WO200216434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
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              10-SEP-2002
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                                                                                                                                                                                                  28-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                               sclerosis
                                                                                                                                                                                                                                                                                                                                       Zhang JZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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basic protein minimal epitope which can be used in a fusion protein of
                                                                                                                                                             Sequence 17 AA;
                                                           the invention
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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     ន្តដ្ឋនូ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                       The present invention relates to glycopeptides (ABR56059-ABR56066). The glycopeptides have high specificity in recognizing autoantibodies involved in multiple sclerosis pathology, and thus are effectively used in diagnosis and treatment for multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising polypeptide sequences that bind to IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP; Reeppilon receptor; autoimmune disease; constent region; heavy chain; antiathmutic; antiallergic; antialler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 94; DB 6; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human myelin basic protein MBP minimal epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA019672 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Fr
                Claim 7; Page 12; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2002; 2002WO-US013527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2001; 2001US-00847208.
24-OCT-2001; 2001US-00000439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-103456/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200288317-A2.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2002
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mediated hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA019672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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The invention discloses a method for inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, comprising administering a composition comprising a peptide analog in combination with a carrier/adjuvant or diluent. The peptide analog comprises at least of amino acids selected from residues 83 to 99 of human myelin basic protein, where: the L-1ysine at position 91, L-arginine at position 95, is altered to another amino acid, and one to L-threonine at position 95, is altered to another amino acid, and one to three L-amino acids selected from valine at position 86 or 87, histidine at position 88, threonine at position 95 or 98, and proline at position of the protein at that position or the L-1ysine at position 91 is altered at protein at that position or the L-1ysine at position 91 is altered to another amino acid and the N- and/or C-terminal amino acid are altered to another amino acid and the N- and/or C-terminal amino acid are altered con another amino acid, such that upon administration of the peptide canalog in vivo proteolysis is reduced. The peptide analog comprises 7-17 amino acids and one to four additional altered residues. The N-terminal contains additional L-amino acids selected from residues 81 to 90 and 92 to 99 to substituted with a charged amino acid. The method is useful for treating multiple sclerosis using peptide analogs of human myelin basic protein. The sequence presented is the wild-type human myelin basic protein. The sequence presented is the wild-type human myelin basic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, useful for treating multiple sclerosis, comprises administering an amount of a pharmaceutical composition comprising a
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Human, Th2; immune response; myelin basic protein; peptide analog;
proteolysis; multiple sclerosis; neuroprotective; gene therapy.
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                    Length 17;
                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                             Wild-type human myelin basic protein peptide analog.
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                Score 94; DB 6;
Pred. No. 7e-09;
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staehelin T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEUR-) NEUROCRINE BIOSCIENCES INC.
100.0%; Sc.__
100.0%; Prev
                                                                                                                                                                                                                                        ADE50773 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00342408.
98US-00137759.
99US-00378244.
                                                                                                1 ENPVVHFFKNIVTPRTP 17
                                                                                                                         ENPVYHEFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ling NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2002; 2002US-00104973
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                            17; Conservative
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                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                      29-JAN-2004
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20-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-2002.
                                                                                                                                                                                                                                                                                  ADE50773;
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100.0%; Score 94; DB 7; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                            ADW36476 standard; peptide; 17 AA.
                                                                                                      1 ENPVOHEFKNIVTPRTP 17
                                                                                                                        Best Local Similarity 100. Matches 17; Conservative
Sequence 17 AA;
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                                 Query Match
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Gaps

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Virucide, cytostatic, gene therapy, vaccine, epitope, cytotoxic T cell, MHC class I; CTL, HTL, A2-restricted cytotoxic lymphocyte, HLA; viral disease; cancer Unidentified. 

10-MAR-2005 (first entry) HLA binding epitope #7226

WO2003040165-A2

15-MAY-2003

18-OCT-2001; 2001WO-US051650.

19-OCT-2000; 2000US-0242350P 20-APR-2001; 2001US-0285624P

EPIM-) EPIMMUNE INC.

Southwood Sidney J, Sette A,

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WPI; 2003-441519/41

New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.

Claim 1; Page 52-379; 382pp; English.

The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MFC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2 reseptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnosing viral diseases and cancer. The peptide point and antibodies and for evaluating efficacy of a vaccine. Sequences given in Tables 2-31.

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Sequence 17 AA;
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Gaps

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100.0%; Score 94; DB 7; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels

1 ENPVOHEFKNIVTPRTP 17 ENPVYHEFKNI VTPRTP 17

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RESULT 11 ADW33812

Query Match
Best Local Similarity 100.0

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                                       Gaps
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100.0%; Score 94; DB 7; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels
                   Best Local Similarity 100.
Matches 17; Conservative
   Query Match
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having an isolated, prepared epitotope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytocoxic T cell response against a pre-selected antigon in a patient expressing a specific MFC class I allele by contacting cytotoxic C composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigon-presenting cell, where when an A2 restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or C diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW29251.
                                                                                                                                                                                                                                                                  Virucide, cytostatic, gene therapy, vaccine, epitope, cytotoxic T cell, MHC class I, CTL, HTL, A2-restricted cytotoxic lymphocyte, HLA, viral disease, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition comprising at least one peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 52-379; 382pp; English.
                                                                                                                        ADW35045 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Southwood S;
                  1 ENPVOHERKNIVTPRTP 17
1 ENPVVHFFKNIVTPRTP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2001; 2001WO-US051650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-OCT-2000; 2000US-0242350P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001US-0285624P
                                                                                                                                                                                              10-MAR-2005 (first entry)
                                                                                                                                                                                                                                HLA binding epitope #5795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sette A, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-441519/41
                                                                                                                                                                                                                                                                                                                                                                              WO2003040165-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2003.
                                                                                                                                                              ADW35045;
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Human; myelin basic protein; vaccine; multiple sclerosis; T cell
                                                            WO2004015070-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 AA;
                                    Homo sapiens.
                                                                                   19-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL18291;
                                                                                                                                                                                                 Zhang JZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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용
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytocoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an apitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HAR molecule on the antigon-presenting cell, where when an A2-restricted cytocoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnosing viral diseases and cancer. The peptide epitopes are useful as and for evaluating efficacy of a vaccine. Sequences given in ADW29231.

ADW37745 represent epitopes of the invention as given in Tables 2-31.
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                                                                                               Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell; MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA; viral disease; cancer.
                                                                                                                                                                                                                                                                                                                                                             New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human myelin basic protein peptide fragment MBP-1 (aal10-126).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 94; DB 7; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 52-379; 382pp; English.
 ADW33812 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                                                                                                  Southwood
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                                                                                                                                                                                                                           18-OCT-2001; 2001WO-US051650.
                                                                                                                                                                                                                                                   19-OCT-2000; 2000US-0242350P.
20-APR-2001; 2001US-0285624P.
                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                         HLA binding epitope #4562
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                                                                                                                                                                                                                                                                                       (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                               Sidney J,
                                                                                                                                                                                                                                                                                                                                        WPI; 2003-441519/41.
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                                                                                                                                                                           WO2003040165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 AA;
                                                                                                                                                 Unidentified.
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                                                10-MAR-2005
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                                                                                                                                                                                                                                                                                                                Sette A,
                        ADW33812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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The present invention is direct to methods of isolating antigen specific CC T cells, especially T cells specific for self or autoantigens. This CC comprises incubating a sample of T cells obtained from a patient with the antigen and selecting T cells that express one or more of first markers cantigen and selecting T cells that express one or more of first markers selected from titerleukin-2, interferon-gamma, tumour necrosis factor alpha, interleukin-2, interferon-gamma, tumour necrosis factor alpha, interleukin-2, interferon-gamma, tumour necrosis factor alpha, interleukin-2, interferon-gamma, tumour necrosis factor alpha, interleukin-10 and interleukin-12. The call squeoise of autoimmune diseases. The methods also permit the disease and for monitoring the efficacy of treatment. The methods also permit the cite allow the preparation of autologous T cell vaccines for the treatment of the disease and for monitoring the efficacy of treatment. The methods also permit interpretation of autologous T cell vaccine preparation involves the specific T cells optionally followed by culturing steps which allow the expansion of the population of isolated antigency specific T cells optionally followed by culturing steps which allow the example from the population of isolated antigency specific T cells for T cell vaccination. Peripheral blood of monouclear cells were isolated from the blood of multiple sclerosis comprises amino acids 10-126 of human myelin basic protein. Cells were comprises amino acids for the expression of gene products indicative of activated from the langered for the expression of gene products indicative of activated from the langered for the expression of gene products indicative of activated from the langered from the l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolating one or more T cells specific for an antigen of interest comprises incubating a T cell sample with an antigen, useful for diagnosing or treating multiple sclerosis, psoriasis, thyroiditie, diabetes and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE. (OPEX-) OPEXA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ENPVYHEEKNIVTPRTP 17
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06-AUG-2003; 2003WO-US024548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-180654/17.
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04-MAR-2004

Vojdani A;

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The invention comprises a method of determining etiology of an autistic spectrum disorder in a patient. The method involves determining the level of an infectious agent, toxic chemical, or dieterry protein derived antigen, or their antibodies in samples of patient, and comparing antigens/antibodies levels with normal levels of antigens/antibodies from control subjects. The method of the invention is useful for determining the etiology of an autistic spectrum disorder, such as autism, pervasive development disorder and Asperger's syndrome. The present amino acid sequence represents a peptide that was used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining etiology of autistic spectrum disorder in patient, by determining level of infectious agent/toxic chemical/dietary protein derived antigen in samples of patient, comparing it with normal level of antigens of control subjects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical; t-lymphocyte; antigen; multiple sclerosis; utcimmune disease; immuned disorder; immune stimulation; immunity; autoimmunity; immunosuppressive; neuroprotective; antiarthritic; antiinflammatory; myelin; myelin basic protein; MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 94; DB 9; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myelin basic protein (MBP) peptide, amino acids 83-99.
       autism; nootropic; asperger syndrome; MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 6; 89pp; English.
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                                                                                                                                                                                                        03-FEB-2004; 2004US-00770712.
                                                                                                                                                                                                                                                       03-FEB-2004; 2004US-00770712.
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                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-562713/57.
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                                                                                                                                                                                                                                                                                                      (VOJD/) VOJDANI A.
                                                                                                         US2005170333-A1
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                                                       Unidentified.
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                                                                                                                                                        04-AUG-2005.
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                                                                                                                                                                                                                                                                                                                                                         Vojdani A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
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AEB86495
AC AEB86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method of diagnosing the likelihood and severity of demyelinating diseases. The method involves determining antibodies against neuron-specific antigen in sample, comparing the level of antibodies with the normal level of antibodies, where normal level of antibodies for the antigen indicate optimal conditions, lower than or higher than normal level of antibodies for the antigen indicate an absence of or a likelihood of demyelinating diseases, respectively. The neuron-specific antigen is chosen from myelin basic protein (MBP), well noligodendrocyte glycoprotein, myelin associated glycoprotein (MAG), proteolipid protein (PLP), small heat shock protein, transaldolase, glial fibrillary protein, S-100 protein, cross-reactive peptide from dietary protein, cross-reactive peptide from infectious agent, glutamate receptor, and phosphodiesterase. The immunoassay is an enzyme linked immunosorbent assay (ELISA) test. The method is useful for disapposing the likelihood and severity of demyelinating diseases such as multiple sclerosis in a patient. The present sequence represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing likelihood and severity of demyelinating disease, by determining antibodies against neuron-specific antigen, comparing level of detected antibodies with normal level for detecting absence/likelihood
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                                                                                                 Demyelinating disease; neuron-specific antigen; human; myelin basic protein; MBP; myelin oligodendrocyte glycoprotein; myelin associated glycoprotein; MAG; proteolipid protein; PLP; small heat shock protein; transaldolase; glial fibrillary protein; S-100 protein; cross-reactive peptide; glutamate receptor; phosphodiesterase; multiple sclerosis.
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Pred. No. 7e-09;
Mismatches 0; Indels
                                                  Human myelin basic protein (MBP), peptide #2.
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Best Local Similarity 100.0%;
Matches 17; Conservative 0
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(first entry)
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                                                                                                                                                                                                                                                                                                                            US2004043431-A1
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  20-MAY-2004
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AEB77584;

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RESULT 14 AEB77584

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(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Houghten RA, Pinilla C, Martin R, Sturzebecher C; Shukaliak-Quandt J, Mcfarland HF;

WPI; 2005-555771/56.

Complex peptide mixture having immunomodulatory effects, useful for preparing medicament for treating autoimmune disease e.g. multiple sclerosis, rheumatoid arthritis, for preparing medicament for stimulating immune cell.

Example; Page 22; 51pp; English

The invention relates to complex peptide mixtures comprises several peptides having 8-20 amino acids, where the mixture comprises peptides having a degree of diversity at defined positions in the peptide chain, where the degree of diversity in the defined position is different from other defined positions, and where in the majority of the mixture, the peptides includes Ala, Glu, Lys and Tyr and no other amino acids, in at least four positions. Also described are: (1) a method of creating a high affinity peptide ligand of a defined formula for a receptor of a T cell that is reactive to a myelin antigen, copolymer, or an active mixture; and (2) a method of enhancing a biological property of a complex mixture of peptides, peptidomimetics, or peptides and peptidomimetics. The complex peptide mixture is useful in the preparation of a medicament for treating a disease such as multiple sclerosis (MS) and experimental aucoimmune encephalomyelities (EAB). It is also useful for preparing a medicament for stimulating an immune cell, or for suppression of an immune reaction (e.g. autoimmune reaction) to an antigen derived from the examples of an encephalomyelities and peptide used in the examples of an encephalomyelities. the present invention. 

Sequence 17 AA;

Gaps ö 100.0%; Score 94; DB 9; Length 17; 100.0%; Pred. No. 7e-09; ive 0; Mismatches 0; Indels Local Similarity 100. Query Match Best Loca Matches

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1 ENPVVHFFKNIVTPRTP 17 ENPVOHEFKNIVTPRTP 17 ò g Search completed: February 22, 2006, 21:30:49 Job time : 14.1572 secs

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                                      February 22, 2006, 21:24:24 ; Search time 154.266 Seconds (without alignments) 1061.041 Million cell updates/sec
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Q5re17
Q86tt2
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     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                    2166443
                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                       2166443 segs, 705528306 residues
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OGGMW7 HUMAN
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Q6N089_HUMAN
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Maximum Match 100%
Listing first 45 summaries
                            - protein search, using sw model
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1: uniprot_sprot:*
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Perfect score:
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32 1123 89.1 509 2 QBNF17 HUMAN QBNF17 homo sapien 34 1107 87.9 326 1 IGHG2 HUMAN QBNF17 homo sapien 35 1107 87.9 326 1 IGHG2 HUMAN QGRUGO sapien 36 1102 87.5 464 2 QGRUGU-HUMAN QGRUGO sapien 37 1102 87.5 465 2 QGRC4-HUMAN QGRUGO sapien 37 1097 87.1 473 2 QBTG4-HUMAN QGRC4 homo sapien 39 1097 87.1 473 2 QBTG4-HUMAN QGRCA homo sapien 41 883 70.1 323 1 GC_RABIT QGRCA homo sapien 42 877.5 69.6 337 QGRAYH-HUMAN QGRCA homo sapien 43 858 68.1 329 1 IGHG2_CAVPO PO1862 cavia porce 44 813 64.5 469 2 QSWB39_RAT QSMB39_rattus norv
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## ALIGNMENTS

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CHOISTHUAN STANDARD; PRT; 330 AA.

MOTOSTICATION STANDARD; MOTOSTICATION Update)

DT 21-JUL-1986 [Rel. 01, Lage sequence update)

DT 21-JUL-1986 [Rel. 04, Lage sequence update)

DT 21-JUL-1986 [Rel. 04, Lage sequence update)

DT 21-JUL-1986 [Rel. 04, Lage sequence update)

E 19 Gamma-1 chain C region.

MORI TEAKID-6606;

RN MORITIAXID-6606;

RN WICLEOTIDE SEQUENCE.

RN WICH AND ALL SEGUENCE TO 1140-129 [RU].

RN WAXAAI MA, L SEGUENCE OF 1-135 (WITELOWA PROTEIN EU).

RN WICLEOTIDE SEQUENCE OF 1136-129 [RU].

RN WICLEOTIDE SEQUENCE OF 1140-129 [RU].

RN WICLEOTIDE SEQUENCE (WYELOWA PROTEIN RUE).

RN WICLEOTIDE SEQUENCE (WYELOWA PROTEIN RUE).

RN WIDLINE-1700-036 PubMede-80415;

RN WIDLIN
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1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                          K -> R (in GlM(3) marker).
/FIId=VAR 003886.
D -> E (in GlM(non-1) marker).
FIId=VAR 003887.
L -> M (in GlM(non-1) marker).
/FIId=VAR 003888.
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                                            Interchain (with light chain).
Interchain (with heavy chain).
Interchain (with heavy chain).
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3; Mismatches 4;
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"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus and 2.9- and 2.9-A resolution.";

Biochemistry 20:2361-2370(1981).

"INSCELLANBOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(1) markers, 23-D and 241-L. KOL and EU sequences have the GIM(1) markers and the GIM (100n-1) markers.

"INSCELLANBOUS: Nie also differs in the amidation states of 35, 16, 179, 198, 269 and 272.

"IS5, 166, 177, 198, 198, 269, and 272 and in the order of residues 268-272.

"INSCELLANBOUS: KOL also differs in the amidation states of residues 268-272.
                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                              MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Breker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The pyrmary structure of a monoclonal IgG1 immunoglobulin (upseloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
         Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds ";
Blochemistry 9:3188-3196(1970).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005624; C:membrane fraction; NAS. GO; GO:0003823; F:antigen binding; TAS. GO; GO:0006955; P:immune response; NAS.
                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE=81208100; PubMed=7236608;
 MEDLINE=71064027; PubMed=4923144;
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PDB; 1AA7; X-ray; H=1-103.
PDB; 1D5B; X-ray; H=1-101.
PDB; 1D5B; X-ray; H=1-101.
PDB; 1D6V; X-ray; H=1-101.
PDB; 1D6V; X-ray; H=1-101.
PDB; 1D6V; X-ray; H=1-101.
PDB; 1EA4; X-ray; A/B=106-329.
PDB; 1FC1; X-ray; A/B=106-329.
PDB; 1FC2; X-ray; A/B=106-329.
PDB; 1FC2; X-ray; A/B=10-329.
PDB; 1TZ; X-ray; A/B=10-330.
PDB; 1TX; X-ray; A/B=119-330.
PDB; 1TX; X-ray; H=1-103.
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X Strausberg R.L., Fedingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Fedingold E.A., Grouse L.H., Derge J.G.,

X Altachur S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A., Rabin G.M., Hong L.,

RA Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glübs R.A.,

R Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R Halton B., Ketteman M.W., Green B.D., Dickson M.C.,

R Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                 278
99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKF 158
                                                                                                        159 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
                                                                                                                                                                            121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                            219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                              NAYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                             181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                            279 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 465 AA, 51083 MW, B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGGMXG;
05-JUJ-2004 (TrEMBLrel. 27, Created)
05-JUJ-2004 (TrEMBLrel. 27, Last sequence update)
05-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC073766; AAH73766.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-21.
InterPro; IPR003596; Ig C1.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig WHC.
InterPro; IPR004596; Ig V.
Pfam; PP07654; C1-8et; 3.
SWART; SW00409; IG; 2.
SWART; SW00407; IGC1; 3.
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TISSUE=Primary B-Cells;
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MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Fealingold E.A., Grouse L.H., Derge J.G.,

Alusaner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Anderstein and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                              ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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   Length 465;
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EMBL; BC072419; AAH72419.1; -; mRNA.
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                    4.
97.2%; Score 1225; DB 2; 97.0%; Pred. No. 9.1e-90; ive 3; Mismatches 4;
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InterPro; IPRO01559; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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   Query Match
Best Local Similarity 97.0
Matches 225; Conservative
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Query Match
Best Local Similarity 97.0
Matches 225, Conservative
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Nauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A ploking R.F., Jordan H., Moore T., Max S.I., Wang J., Heibe F.,
A papleron M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Tonahlyuki S., Carninci P., Frange C.,
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Brownstein M.J., Waln P.B., Peters G.J., Abramson R.D., Mullahy S.J.,
Brokesk S.A., McKwan P.J., McKernan R.J., Malek J.A., Gunzarne P.H.,
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakebley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                           Length 466;
                                                                                                                                                                                                      Indels
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EMBL; BC092518; AAH92518.1; -; mRNA.
SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
                SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50220; IG MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50854 MW; 53EB0BCEDEB1076E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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                                                                                                                                                      Score 1225; DB 2;
Pred. No. 9.1e-90;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                           97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q569F4_HUMAN PRELIMINARY;
Q569F4;
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SMART; SM00409; IG; 2.
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NUCLEOTIDE SEQUENCE.
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Name=IGHG1;
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TISSUE-Spleen,
WEDLINE-2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
WEDLINE-2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
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Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Control of M. M. All A., John J. J., Marra M.A.,
C. Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Last sequence update)
Last annotation update)
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97.2%; Score 1225; DB 2;
97.0%; Pred. No. 9.2e-90;
tive 3; Mismatches 4;
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EMBL, BCO51328, AAH51328.1; -; mRNA.
HSSP, PO1857; HZM.
SWR, Q727P5; 20-469.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003696; Ig.MHC.
InterPro; IPR003596; Ig. Prof. InterProf. Inte
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Q7Z7PS;
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01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Name=IGHG1;
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                                                                             Query Match
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                                                                                              EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297
                                                                                                                     NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                      357
                                                                                                                                                      121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                       417
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                              298 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                358 ISKAKGQPREPQVYILPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTP
                                                                                    1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                      PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                              PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                  Query Match 97.2%; Score 1225; DB 2; Length 469; Best Local Similarity 97.0%; Pred. No. 9.2e-90; Matches 225; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053984; AAH53984.1; -; mRNA.
HSSP; P01857; 1HZH.
                                    51395 MW; C8D5BE12BAAF795C CRC64;
                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                470 AA
SMART, SM00406, IGV; 1.
PROSITE, PS50835; IG_LIKE, 4.
PROSITE, PS00299; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                  Created)
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InterPro; IPR003597; Ig_c1.
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                                                                                                                                                                                                                                                Q7Z5W1 HUMAN PRELIMINARY;
Q7Z5W1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
                        Immunoglobulin domain.
SEQUENCE 469 AA; 51
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MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
Blackhenko L., Marushina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,
Butterfield Y.S.N., Marra M.A.;
Butterfield W.B., Marra M.A.;
Butterfield W.B., Marra M.A.;
Butterfield Y.S.N., Marra M.A.;
Butterfield W.B., Marra M.A.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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TISSUE-Primary B-Cells;
NIH MGC Project;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                               InterProj IPR003596; Ig_v.
Pfam; PP07654; CL-set; 3.
SMART, PR07654; CL-set; 3.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00290; IG_MC; UNKNOWN 2.
Hypochetical protein; Immunoglobulin domain.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                Score 1225; DB 2;
Pred. No. 9.2e-90;
                                                                                                                                                                                                                                                                                                                                                97.2%; Scur.
97.0%; Pred. No. >...
3; Mismatches
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InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                   361 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 420
                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                  61 NWYUDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMYGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                          121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                              1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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Gaucher C., Klein P., Beliard R.;
"Sequence determination of the recombinant human anti-RhD moncation of Tallibody T122."

I antibody T122."

Submitted (JAN-205) to the EMBL/GenBank/DDBJ databases.

R EMBL; AY894992; AAW82028.1; -; mRNA.

RINTERPRO; IPR001359; Ig_C1.

R InterPro; IPR001359; Ig_C1.

R InterPro; IPR001306; Ig_MHC.

R InterPro; IPR001306; Ig_WHC.

R Ffam; PF07684; C1-set; 3.

R SWART; SW00409; IG; 2.

SWART; SW00409; IG; 2.

R PROSITE; PS50835; IG_LIKE; 4.
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                             Length 472;
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                                                                              Indels
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sentotation update)
Anti-RhD monoclonal T125 gammal heavy chain precursor.
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97.0%; Pred. No. 9.3e-90;
ilve 3; Mismatches 4;
                          Score 1225; DB 2;
Pred. No. 9.2e-90;
          97.2%; Scor.
97.0%; Pred. No. 5.2.
3; Mismatches
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                                                   Best Local Similarity 97.0 Matches 225; Conservative
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SIGNAL
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G. Tissubsractum, Cumca, C. Tissubsractum, C. The German cDNA Consortium;
A Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;
L. Submitted (JAN-2015) to the EMBL/GenBank/DDBJ databases.
I. BMBL; BX640627; CAR45781.1; -; mRNA.
I. BMBL; BX640627; CAR45781.1; -; mRNA.
I. RICHPTO; IPR0013597; IQ.C1.
IN InterPro; IPR0013597; IQ.C1.
IN InterPro; IPR0013597; IQ.C1.
IN InterPro; IPR001356; IQ.V.
IN EMMRT; SM00405; IG.2.
IN SWART; SM00406; IG.2.
IN SWART; SM00406; IG.1; 3.
IN SWART; SM00406; IG.1; 3.
IN PROSITE; PS00290; IG LIKE; 4.
IN PROSITE; PS00290; IG LIKE; 4.
INCOLLANT, CALL INTERPORTED INTERPRORTED INTERPORTED INTERPRORTED 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 97.2%; Score 1225; DB 2; Length 470; Local Similarity 97.0%; Pred. No. 9.2e-90; nes 225; Conservative 3; Mismatches 4; Indels (
EMBL; BC018747; AAH18747.1; -; mRNA.

HSSP; PO1861; 1ADQ.

SMR; Q6PJA4; 20-47.

InterPro; IPR001359; Ig.

InterPro; IPR003006; Ig_MG.

InterPro; IPR003006; Ig_WHC.

InterPro; IPR003596; Ig_W.

Refan; PP07654; C1-set; 3.

SMART; SM00409; IGC, 2.

SMART; SM00409; IGC, 2.

SMART; SM00409; IGC, 2.

REART; SM00409; IGC, 1.

REART; SM00406; IGV; 1.

REART; SM00409; IG_MRC; UNKNOWN 2.

REQUENCE 470 AA; $\frac{1}{5}$116 MW; 7849556A1IFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 protein. - 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686F15220.
Name=DKFZp686F15220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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QGN089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
TISSUE=Rectum tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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SEQUENCE 47
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Matches
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MEDINESIDE SPECENCY OF THE STATE OF THE SCHOOL OF THE STATE OF THE STA
                                                                                                                                                                      ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                            304 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                    364 ISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                        424 PVLDSDGSFFLYSKITVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
                                                                                                                                                                                                                                                                                                             PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Strausberg R.; Strausberg G.; Strausberg G.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BCO73773; AAH73773.1; -; mRNA. GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.2%; Score 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | InterPro; | Cititudgrain of membrane | InterPro; | PR001559; | 19-11ke. | InterPro; | PR001599; | 19-11ke. | InterPro; | PR001599; | 19-11ke. | InterPro; | PR001599; | 19-11ke. | InterPro; | PR0013006; | 19-MHC. | InterPro; | PR0013006; | 19-MHC. | InterPro; | PR001596; | 19-NHC. | InterPro; | PR001596; | 10-NHC; | SWART; | SM00400; | 10-13 | SWART; | SM00400; | 10-NHC; | 10-NHC; | PR0017E; | PS00190; | 10-MHC; | UNKNOWN_2. | PR0517E; | PS00190; | 10-MHC; | UNKNOWN_2. | Hypothetical procein. | SEQUENCE | 476 AA; | 52286 WW; | 622AABA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGGMX1_HUMAN PRELIMINARY;
QGGMX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
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244 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                    PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNYQQRSLSLSPGK 232
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Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO13782; AAH73782.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51987 MW; 2A1FE55D736860F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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97.2%; Score 1225; DB 2;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                        475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001359; IG.
InterPro; IPR00110; Ig-11ke.
InterPro; IPR003109; Ig. C1.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.MHC.
Pfam; PF07654; C1-8et; 3.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                     QGGMW7_HUMAN PRELIMINARY;
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TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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OGGNW7 HUAN

OGGNW7 HU-20

DT 05-UUL-20

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Gaps

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180 627

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TISSUE-PETIDHEAL NETWOUS SYSTEM;

TALGEBOOK R.L., Fallgold E.A., Groude L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab S.S., Loquellano N.H., Peters G.J., Abramson R.D., Mullahy S.J.,

Rab S.S., Worlev N., Pokernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worlev K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worlev A., Young A.C., Shevchenko Y., Bouffard G.G.,

Nilling M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Rochert A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 679;
                 SWART; SMOO407; IGC1; 1.

SWART; SMOO407; IGC1; 1.

SWART; SMOO120; Tryp SPC; 1.

PROSITE; PSO0100; ASX HYDROXYL; UNKNOWN_1.

PROSITE; PSO1186; EGF 2; 1.

PROSITE; PSO1018; EGF 2; 1.

PROSITE; PSO1019; IG M-1; UNKNOWN_1.

PROSITE; PSO1019; IG M-1; UNKNOWN_1.

PROSITE; PSO1019; IG M-1; UNKNOWN_1.

PROSITE; PSO1019; IRYPSIN DOM; 1.

PROSITE; PSO1013; TRYPSIN DOM; 1.

PROSITE; PSO1013; TRYPSIN JESP; 1.

SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;
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Last annotation update)
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Pred. No. 1.5e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 225; Conservative
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Best Local Similarity
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MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
Hu Z., Garen A.;
"Targeting transport factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                   61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                          305 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                  1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                      Gaps
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Submitted (FRB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF272774; AAK58686.2; -; mRNA.
HSSP; P08709; 1KLI.
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GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IER000152; Asx_hydroxyl_S.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Factor VII active site mutant immunoconjugate.
Homo sapiens (Human)
   Pred. No. 9.3e-90; 3; Mismatches 4
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InterPro; IPR001254; Peptidase_S1_S6.
InterPro; IPR002034; VitK_dep_GIA.
Pfan; PP07654; C1 set; 2.
Pfan; PF00008; EGF; 1.
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR005209; EGF_II.
InterPro; IPR007100; IG_II.
InterPro; IPR003597; IG_II.
InterPro; IPR003597; IG_II.
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Pfam; PF00059; Txypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00001; GLABLOOD.
97.0%;
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Q96PQ8;
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                            225; Conservative
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   Local Similarity
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                                   Matches
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244 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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The German cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger .
Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640622; CAE45776.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEGLHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                              Length 475;
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                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                              SWART; SW00409; IG; 2.
SWART; SW00409; IGG1, 3.
SWART; SW00406; IGG1, 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypochhetical protein:
SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686001196.
                                                                                                                                                                                                                                                                                                                  Query Match 96.9%; Score 1221; DB 2; Best Local Similarity 96.6%; Pred. No. 1.9e-89; Matches 224; Conservative 3; Mismatches 5;
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-21.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_V.
Pfam; PP00564; C1-set; G.
SWART; SW00409; IG; 2.
SWART; SW00407; IGC1; 3.
SWART; SW00407; IGC1; 3.
PROSITE; PS00290; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Q6N094;
   Pfam; PF07654; C1-set; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKT 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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TISSUB-Esophagus tumor;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo (Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640947; CAE45972.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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A STRAUBBERG R.;
Straubberg R.;
Submit GUAN-2014) to the EMBL/GenBank/DDBJ databases.

R Submit BCG6520, AA465820.1; -; mRNA.

R HSSP; P01861; 1ADQ.

R InterPro; IPR001359; IG.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR003597; Ig.

R InterPro; IPR003597; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R SMART; SMO0409; IG.1.3.

R SMART; SMO0409; IG.1.3.

R SMART; SMO0409; IG.1.3.

R SMART; SMO0409; IG.1.3.

R SMART; SMO0409; IG. IG.

R PROSITE; PS00299; IG. MHC; UNKNOWN_2.

HYPOCHELICAL PROCEEN.

R SKQUENCE 473 AA; S1344 WW; 9816D56A77129B57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
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OSGMZQG_
OS-JUL-2004 (TrEMBLrel. 27, Created)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein DKFZp686G11190.
Name=DKFZp686G11190;
                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
96.9%; Score 1221; DB 2;
Best Local Similarity 96.6%; Pred. No. 1.9e-89;
Matches 224; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
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InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig WHC.
mouse cDNA sequences.";
                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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AC 066M206
AC 066M20
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249 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKF 308
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Search completed: February 22, 2006, 21:37:12 Job time : 154.266 secs

Appli Appli

Sequence 7, A Sequence 25, Sequence 25, Sequence 14, Sequence 16, Sequence 18, Sequence 18, Sequence 14,

Sequence Sequence S

Sequence 2, 1 Sequence 2, 1 Sequence 14,

Sequence

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Sequence 7, Application US/08236311
Patent No. 556533
GENERAL INFORMATION
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDERE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STRATE: California
COUNTY: USA
ZIP: 94000
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CONFUTER: IBM PC Compatible
CONFUTER: IBM PC Compatible
CONFUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patla (Genentech)
CONFUTER: 10 PATL (Genentech)
CONFUTER: 10 PATL (ATTON DATA:
APPLICATION NUMBER: 05/936190
FILING DATE: 26-AUG-1992
RIGH APPLICATION NUMBER: 07/250785
FILING DATE: 28-ESP-1988
FILING DATE: 28
US-09-526-098-8

US-09-318-316-8

US-09-758-173-8

US-09-756-424-8

US-09-157-101A-7

US-09-740-002-25

US-09-740-002-25

US-09-807-352B-14

US-08-807-352B-14

US-08-807-352B-16

US-08-466-151-65

US-09-109-207C-16

US-09-109-207C-16

US-09-109-207C-18

US-09-109-207C-18

US-09-109-207C-18

US-09-109-207C-18

US-09-109-207C-18

US-09-109-207C-18
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US-08-236-311-7
 1725
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    Sequence 13, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 54, Appl
Sequence 53, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 4, Appli
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12, Appl
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                                                                                                    February 22, 2006, 21:37:34; Search time 49.0155 Seconds (without alignments) 556.619 Million cell updates/sec
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Sequence 12,
Sequence 4, A
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Sequence 7, 1
Sequence 7, 1
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                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-458-516-13

US-08-030-175-41

US-08-030-175-42

US-08-030-175-42

US-08-378-939-10

US-09-376-359A-54

US-09-313-942-9

US-09-313-942A-7

US-09-313-942A-7

US-09-440-002-27

US-09-740-002-27

US-09-740-002-27

US-09-740-002-27

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US-09-740-002-27

US-09-750-4

US-09-750-12
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                                                                                                                                                                                                                                                                             572060 seqs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1764
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Match Length
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Perfect score:
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PSVPLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVDGVEVHNVKTKPREEQYN 180
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                                                                                                                                                                                                                                                                   Length 371;
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER: READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datin (Genenech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,408
FILING DATE: 28-May-2002
FILING DATE: 28-May-2002
FILING DATE: 1-UNY-1995
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-UNY-1995
APPLICATION NUMBER: 07/936190
                                                                                                                                                                                                                                                                 Score 1729; DB 2;
Pred. No. 1.1e-156;
3; Mismatches 4;
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Sequence 7, Application US/10157408

Patent No. 6710169

GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.

Gregory, Timothy J.

TITLE OF INVENTION: Adheson Variants

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 OCGNVFSCSVMHEALHNHYOORSLSLSPGK 330
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                   P0444P1C3
            REFERENCE/DOCKET NUMBER: P044,
TELECOMUNICATION INFORMATION:
TELEPAX: 415/952-981,
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYRE: amino acid
TOSE-08-457-918-7
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative 3
REGISTRATION NUMBER:
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182 LIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLIVDKSRM 341
                                                                                                                                                                                                             120
                                                                                                                                                                                                                                     102 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVPPKSCDKTHTCPPCPAPELLGG 161
                                                                                                                                              42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101
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                                                                                                                                                                                                                                                                                                                                                                             STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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                                                                                                                                                                                                             GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                    Gaps
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                                    Length 371;
                                                                                  4; Indels
                                      Score 1729; DB 1;
Pred. No. 1,1e-156;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILLING DATE: 1-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08457918; Patent No. 6117655; GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
FILING DATE: 07/936190
FILING DATE: 26-AUG-1992
FILING DATE: 26-AUG-1992
FILING DATE: 26-AUG-1992
FILING DATE: 26-AUG-1992
FILING DATE: 18-FEB-1992
FILING DATE: 19-FEB-1992
FILING DATE: 19-SEB-1992
FILING DATE: 28-SEP-1988
FILING DATE: 28-SEP-1988
FILING DATE: 20-SCT-1987
APPLICATION NUMBER: 07/104329
FILING DATE: 20-CGT-1987
ATTORNEY/AGENT INFORMATION:
NAME: KUDINGC, Jeffrey S.
                                           98.0%;
                                      Query Match
Best Local Similarity 97.9
Matches 323, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-457-918-7
    US-08-236-311-7
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Length 446;
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Sequence 13, Application US/08458516;
Patent No. 5777085;
GENERAL INFORMATION:
APPLICANT: Co., Man Sung;
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA;
NUMBER OF SEQUENCES: 23;
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000;
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
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                                                                                                                                                                                                                           PRIOR APPLICATION: A24
PRIOR APPLICATION NDATA:
APPLICATION NDMBER: US 07/859,583
FILING DATE: 27-AAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,123
TELEPHONE: 415-326-2400
TELEFAX: 416-326-2400
TELEFAX: 416-326-3400
TELEFAX: 416-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-397-411-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                           FILING DATE: 01 CLASSIFICATION:
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US-08-458-516-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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; Patent No. 6129914
; GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
TITLE OF INVENTION: B-Specific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
CITY: California
COUNTRY: USA
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98.0%; Score 1729; DB 2;
Best Local Similarity 97.9%; Pred. No. 1.1e-156;
Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET WUMBER: P0444PIC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OCCNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                      APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
FILING DATE: 26-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 371 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID 0: 7:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-397-411-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 STYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356
                                                                                                                                                                                                                                                  61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                  1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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198 GLYSLSSVVTVPSSSLGTQTYICHVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 257
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Patent No. 6767996

GENERAL INFORMATION:
APPLICANT: Clark, Michael R.
APPLICANT: Clark, Michael R.
APPLICANT: Chark, Michael R.
APPLICANT: Maldmann, Herman
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
MUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
STREET: 555 13TH ST., NW Suite 701 Bast
CITY: Washington
STATE: D. C.
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                                                   Kb storage
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    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb COMPUTER: IBM AT compatible OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2 SOFRANING SYSTEM: US/08/030,175 FLING DATE: US/08/030,175 FILING DATE: US/08/030,175 FILING DATE: 13-SEP-1991 ATTORNEY/AGENT INFORMATION: NAME: ETHER, BATDARA G. REGISTRATION NUMBER: 30,377 REFERENCE/DOCKET NUMBER: 1768-113 TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELECOMUNICATION SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acide TYPE: amino acide TTORE: minear TYPE: minear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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APPLICANT: Clark, Michael R.
APPLICANT: Clark, Michael R.
APPLICANT: Cobbold, Stephen P.
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
STREET: 555 13TH ST., NW Suite 701 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIPICATION: 424
PRIOR APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-326-2422
INFORMATION FOR EGO ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TTYPE: AUTONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.0%; Score 1729; DB 1; Best Local Similarity 97.9%; Pred. No. 1.5e-156; Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Patent No. 6767996
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D. C. COUNTRY: U.S.
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US-08-030-175-41
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201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 LIKNQVSLICLUVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLIVDKSRW 440
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                                                                                                                Length 470;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                             Query Match 98.0%; Score 1729; DB 2; Best Local Similarity 97.9%; Pred. No. 1.6e-156; Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08378939;
Patent No. 5876961;
GENERAL INFORMATION: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER;
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES;
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, PIGG, ERNST & KURZ
STREET: STREET: SES THIRTEENTH ST. N.W.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (202) 783-6040
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                                         ; ORGANISM: Homo sapiens
US-10-104-047-3730
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US-08-378-939-10
LENGTH: 470
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         CONTUTER READABLE FORM:

MEDIUM TYPE: 18M AT compatible
COMPUTER: WordPerfect 5.0 (Dos Text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175
FILING DATE: 17-MAY-1993
CLASSIFICATION: 424
RELOR APPLICATION: 424
RELOR APPLICATION: A124
APPLICATION: A24
RELOR APPLICATION: A134
REPERENCE/DOCKET NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 30,377
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
TELECOMPUTER: CA202783-6040
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTER.ESTICE:
LENGTH: 467 amino acids
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; Sequence 3730, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
   APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION UNBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3730
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TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 97.99
Matches 323; Conservative
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US-10-104-047-3730
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61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                                                                                                                                                                                LIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSVGSFFLYSKLTVDKSRW 300
                   278 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                        458 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
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                                                                            PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
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APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 67775394k, Julia E.
APPLICANT: No. 67775394k, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHAII CYTOKINE RECEPTORS: FILE REFRENCE: 00-22
CURRENT APPLICATION NUMBER: US 60/194,731
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR PILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 567
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-825-561A-16
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98.0%; Score 1729; DB 2;
Best Local Similarity 97.9%; Pred. No. 2.1e-156;
Matches 323; Conservative 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 16, Application US/09825561A; Patent No. 6777539
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                                                                                                                                                                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                               327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
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                                                                              Length 476;
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                                                                                                                          4; Indels
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JOHNEACH INFORMATION:

APPLICANT: Ku, wenfeng
APPLICANT: Ku, wenfeng
APPLICANT: Ku, wenfeng
APPLICANT: Kelly, James D.
APPLICANT: Began, Maribeth A.
APPLICANT: Bagan, Maribeth A.
APPLICANT: Bagan, Maribeth A.
APPLICANT: Bagan, Maribeth A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 66102864, Julia E.
FILE REFERENCE: 99-108
FILE REFERENCE: 99-108
CURRENT PLING DATE: 2001-05-21
FRIOR APPLICATION NUMBER: 60/171,969
FRIOR FILING DATE: 1999-12-23
FRIOR FILING DATE: 1999-12-23
FRIOR APPLICATION NUMBER: 60/213,341
FRIOR APPLICATION NUMBER: 60/213,341
                                                                              Score 1729; DB 1;
Pred. No. 1.6e-156;
3; Mismatches 4;
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3; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
                                                                              Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative 3
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Matches 323; Conservative
t TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-939-10
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241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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Sequence 9, Application US/10282162
Sequence 9, Application US/10282162
Sequence 9. Application US/10282162
Sequence 9. Application US/10282162
Sequence 9. Application US/10282162
SEREAL INFORMATION:
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF WAKING
TITLE OF INVENTION: ADD USING
STILE REFERENCE: REG 200-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-09-22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 951
TYPE: PRT

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TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING FILE REFERENCE: REG 203-A CURRENT APPLICATION NUMBER: US/09/313,942 CURRENT FILING DATE: 1999-05-19 PRIOR APPLICATION NUMBER: 09/313,942 PRIOR APPLICATION NUMBER: 60/101,858 PRIOR APPLICATION NUMBER: 60/101,858 PRIOR APPLICATION NUMBER: 60/101,858 PRIOR APPLICATION NUMBER: 60/101,858 NUMBER OF SEQ ID NOS: 32 SOFTWARE: FRANKE: 
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Pred. No. 4.6e-156;
3; Mismatches 4;
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Best Local Similarity 97.9%;
Matches 323; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Foster, Donald C.
APPLICANT: Town whefeng
APPLICANT: Xu, Wenfeng
APPLICANT: Xu, Wenfeng
APPLICANT: Xu, Wenfeng
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Bagan, Maribeth A.
APPLICANT: Bagan, Maribeth A.
APPLICANT: Candraeskher, Yasmin A.
APPLICANT: Candraeskher, Yasmin A.
APPLICANT: Os. 6610286ak, Julia E.
TILLE REFERENCE: 99-108
CURRENT APPLICANTON: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR APPLICATION NUMBER: 2000-06-22
NUMBER OF SEQ ID NOS: 72
LENGTH APPLICATION NUMBER: 2000-06-22
ILENGTH APPLICATION NUMBER: 2000-06-22
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98.0%; Score 1729; DB 2;
Best Local Similarity 97.9%; Pred. No. 2.1e-156;
Matches 323; Conservative 3; Mismatches 4;
                                                                   301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                            538 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
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Patent No. 6472193
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 53, Application US/09746359A
Patent No. 6610286
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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| Sequence 7, Application US/09289942A
| Patent No. 6482928
| GENERAL INFORMATION:
| APPLICANT: Pai, Emil F.
| APPLICANT: Chong, Pele
| APPLICANT: Pedyczak, Arthur
| TITLE OF INVENTION: MONOCLONAL ANTIBODY ZF5
| TITLE OF INVENTION: MONOCLONAL ANTIBODY ZF5
| CURRENT APPLICATION NUMBER: US/09/289,942A
| CURRENT FILING DATE: 1999-04-13
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 7
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                           681
                                                         GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
                                                                      PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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                                                                                                                                                                                        STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 861
                ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
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US-09-289-942A-7
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Db 433 QQGNVFSCSVMHBALHNHYTQKSLSLSPGK 462
Search completed: February 22, 2006, 21:39:48
Job time : 50.0155 secs
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February 22, 2006, 21:24:11; Search time 216.58 Seconds (without alignments) 669.475 Million cell updates/sec
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1764
1 ASTKGPSVPPLAPSSKSTSG.......MHEALHNHYQQRSLSLSPGK 330
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result	3000	Query	1 1 1	2	1	, to 200
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н	1764	100.0	330	9	AA019664	Aao19664 Human IgG
7	1732	98.2	330	σ	ADZ69628	Adz69628 Human IgG
m	1729	98.0	330	4	AAB04071	Aab04071 Zcytor 10
4	1729	98.0	330	Ŋ	AAM47856	Aam47856 Human Ig-
S	1729	98.0	330	Ŋ	AAE21960	Human
9	1729	98.0	330	Ŋ	ABB81641	Abb81641 Human IgG
7	1729	98.0	330	Ŋ	ABB05736	
80	1729	98.0	330	9	ABP71856	Abp71856 Human IgG
თ	1729	98.0	330	ø	AAE32915	Human
10	1729	98.0	330	9	AAE32627	Aae32627 Human imm
11	1729	98.0	330	9	ABR82103	Abr82103 Human DR6
12	1729	98.0	330	9	AA031102	Aao31102 Human A2-
13	1729	98.0	330	9	ABR55836	Abr55836 Anti-Ang-
14	1729	98.0	330	9	AA030893	
15	1729	98.0	330	7	ADF11389	Adf11389 Anti-OPGL
16	1729	98.0	330	7	ADE97351	
17	1729	98.0	330	7	ADF83605	Adf83605 Cytokine
18	1729	98.0	330	7	ADF75001	Adf75001 Human Ig
19	1729	98.0	330	æ	ADM41537	Adm41537 Anti-inte
20	1729	98.0	330	æ	ADM68911	Adm68911 Human IgG
21	1729	98.0	330	œ	ADR43460	Heavy
22	1729	98.0	330	œ	ADR31605	
23	1729	98.0	330	80	ADS87909	Ads87909 Anti-IFN-
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Adn33230 IgG1-CH h

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Ad894906 Anti-IFN- Ad833009 Human IgG Ad833009 Human IgG Ad5577 Heavy cha Ad51577 Heavy cha Ad51581 Heavy cha Ad51581 Heavy cha Ad68015 Muman Hul Ad080657 Human Im Adw8657 Human IgG Ady98273 Human IgG Ady98273 Human IgG Ady5687 Human IgG Ady5688 Human IgG Ady5688 Human IgG Ady5688 Amino aci Aea25942 Human IgG Aea25942 Human IgG Aea25942 Human IgG Aea26942 Human IgG Aea26948 Amino aci Aec08181 Heavy cha Ad135095 Human IgG Adv75455 Human IgG	ALIGNMENTS  0 AA.  t region.  immunotherapy; immune disease; disease; constant region; heavy chain; ntiinflammatory; dermatological; antidiabetic; neuroprotective.	omprising polypeptide sequences that bind to IgG d native IgE receptor, useful for treating IgE- ity reactions, e.g. asthma or allergies, or  ; English.  relates to a fusion molecule comprising a first apable of specific binding to a native IgG nsisting of an immune receptor tyrosine-based b), expressed on mast cells, basophils or B cells, to a second polypeptide sequence capable of ty or indirectly to a native IgE receptor vided are nucleotide sequences encoding such a sion molecules and compositions are useful for
B ADS94906 B ADT333009 B ADT818769 B ADT815157124 B ADT81724 B ADT81724 B ADT81724 B ADT81724 B ADT81724 B ADT81724 B ADT81726 B ADT81725 B ADT81725 B ADT81726	33 33 7	NPI; 2003-103456/09.  New fusion molecules comprising polinhibitory receptor and native Igs mediated hypersensitivity reactions autoimmune diseases.  Claim 64; Fig 2; 116pp; English.  The present invention relates to a polypeptide sequence capable of speinhibitory receptor consisting of a inhibitory motif (ITIM), expressed functionally connected to a second specific binding directly or interference of the second functionally connected to a recond specific binding directly or indire (FcepsilonR). Also provided are nucfusion protein. The fusion molecule
	(first entry) avy chain consimmunoglobulin ceptor; autoimm; antiallergic;; antirheumatic;  2002WO-US01352 2001US-00847201 2001US-000004352 california.	WPI; 2003-103456/09.  New fusion molecules compinhibitory receptor and nawdiated hypersensitivity autoimmune diseases.  Claim 64; Fig 2; 116pp; E The present invention religious encloyepeticle sequence capalinhibitory receptor constinhibitory motif (ITIM), inhibitory motif (ITIM), specific binding directly specific binding directly (RecpsilonR). Also provid fusion protein. The fusion
	tan  11, rec  rec  tic  tic  7-A  7-A  11, 11, 11, 11, 11, 11, 11, 11, 11, 1	fusion molecules bitory receptor ated hypersensit immune diseases.  m 64; Fig 2; 116 present inventio peptide sequence bitory receptor bitory motif (IT tionally connect invally connect inconally connect pailons). Also pon protein. The
6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		New fusion inhibitor mediated autoimmun Claim 64; The presen polypeption inhibitor; inhibitor; inhibitor; inhibitor; functiona specific as precession fusion preference in fusion preference in function fusion preference in fusion preference in fusion preference in fusion preference in function fusion preference in fusion pr
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           hypersensitivity reaction, such as asthms, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgG1
preferably an IgE-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   engineering;
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                                                                                                                                                                Length 330;
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4.6e-125;
an IgE-mediated biological response,
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100.0%; Pred. No. 4.6
tive 0; Mismatches
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14-APR-2004; 2004US-0562627P.
                                                                                                        heavy chain constant region
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                                                                                                                                                                                                Conservative
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Misc-difference
                                                                                                                                     Sequence 330 AA;
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The interior istance to a modulative form the process of a main acid residue from the heavy chain constant region selected from residues 250, 314, and 428 (Kabat numbering) is different from that present in the unmodified Fc-fusion protein. Also included are an Fc-fusion protein comprising an Fc region substantially identical to that of a naturally occurring class IgG antibody, a modified Fc-fusion protein court in that of the corresponding unmodified Fc-fusion protein, a modified IgG class antibody fragment (comprising a heavy chain constant region or Fc-region where at least one amino acid residue selected from the group consisting of residues 250, 314, and 428 is different from that present in the unmodified IgG class antibody), an isolated polynucleotide molecule encoding a polypeptide comprising a sequence at least 90% identical to a sequence selected from ADZ69656, an isolated polypeptide comprising an amino acid sequence at least 90% identical to sequence selected from ADZ69656, an method for altering FcRn binding at least one amino acid seduce as cited above, and substituting the selected residue(s) with an amino acid different from chair present in the Fcfusion protein) and a method of producing a modified Fc-fusion protein with an amino acid sequence FCFusion protein with an amino acid sequence of Erchain with an altered binding affinity for FCRN/altered servum half-life as compared with the unmodified Fc-fusion protein with the unmodified Fc-fusion protein with the unmodified Fc-fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein (comprising preparing an expression vector comprising a suitable promoter operably linked to DNA encoding at least a constant region of an 1967 heavy chain, transforming host cells with the vector and culturing the transformed host cells to produce the modified 196 Fc fusion protein). The modified antibody has a higher affinity for FcRn at DH 6.0 than at DH 8.0. The fusion proteins are useful for studying protein gentcion in vitro and in vivo and as potential therapeutic and diagnostic agents. The present sequence represents a human 1961 heavy chain constant region with an amino acid substitution at residue 250, 314 or 428 (Kabat numbering, the actual residue that is mutated is covered in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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                                                              New modified Fc-fusion protein where at least one amino acid residue from
the heavy chain constant region, useful for studying protein function in
vitro and in vivo and as potential therapeutic and diagnostic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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                                                                                                                                                                                                       invention relates to a modified Fc-fusion protein where at least
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98.2%; Score 1732; DB 9;
Best Local Similarity 98.2%; Pred. No. 1.2e-122;
Matches 324; Conservative 2; Mismatches 4;
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                    WPI; 2005-315683/32.
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61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG

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121 PSVFLFPPKPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN

LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300 

STYRVVSVLTVLHQNWMGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE

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soluting a nucleotide which encodes the zcytor 10 cytokine receptor enables the production of recombinant cells expressing the receptor.

Those cells can then be used to detect the presence of a modulator of zcytor10 protein by culturing the cells in the presence of a test ligand and comparing levels of activity of mouse zcytor10 in the presence and absence of the test sample. Similarly, detection of zcytor10 receptor ilgand within a test sample can be achieved. The method comprising contacting a test sample can be achieved. The method comprising contacting a test sample containing an amino acid sequence from Cysls or divys to Pro230 of the zcytor 10 cytokine receptor and detecting the binding of the polypeptide to a ligand in the sample. Specified peptide fragments of the zcytor 10 cytokine receptor and the methods described are used to identify ligands that stimulate the proliferation and/or development of haematopoietic, lymphoid and mycloid cells. Peptide fragments of the cytokine receptor are useful for treating lymphoid, immune, inflammatory, splenic, blood or bone disorders and for generating continuants of the cytokine receptor. A vector expressing a secreted human zcytor 10 heterodimer is constructed. In this construct the cytokine receptor subunit gamma and the extracellular portion of the the heteromeric cytokine receptor subunit (an interleukin receptor subunit) is fused to human xappa light chain (see GBNESEQ record AAAS4474). The two sequences are fused together using two primers (AAAS4475, AAAS4476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cytokine receptor mouse zcytor 10, useful for detecting ligands that stimulate proliferation or development of hematopoietic, lymphoid and myeloid cells.
                                                                                                                                                                                         zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand; binding; detection; modulation; recombinant cell; haematopoietic cell; lymphoid cell; myeloid cell; lymph; lwmune system; blood; bone; inflammator; response; inflammation; spleen; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indele (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 17; Page 120-121; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Presnell SR, Foster DC, Hammond AK,
                                                                                                                                                 Zcytor 10::IgG gamma fusion peptide.
             AAB04071 standard; protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2000; 2000WO-US012924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00309861.
                                                                                                   11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-016096/02.
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                                                                                                                                                                                                                                                                                                                                                                         WO200068381-A1
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-2000
                                                                                                                                                                                                                                                                                                        Synthetic
                                                            AAB04071;
AAB0407
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Human; immunoadhesin; intercellular adhesion molecule; ICAM-1; human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;

transgenic plant.

Homo sapiens.

WO200183529-A2.

08-NOV-2001.

(PLAN-) PLANET BIOTECHNOLOGY INC. 28-APR-2000; 2000US-0200298P. 28-APR-2001; 2001WO-US013932.

Larrick JW, Wycoff KL;

Human Ig-gammal heavy chain constant region amino acid sequence.

(first entry)

22-FEB-2002

AAM47856;

AAM47856 standard; protein; 330 AA.

AAM47856 ID AAM4 RESULT 4

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The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin is useful for educing infection and virucide activity. The immunoadhesin is useful for equicing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and release of the infectivity, competing with cell surface ICAM-1 for binding release interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effectives of the immunoadhesin. Association of secretory component and immunoglobulin J immunoadhesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 7; 138pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    component in association.
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N-PSDB; ABA05265.
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Gaps ö 9 9

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS

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WPI; 2002-351283/38.
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ABB81641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
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chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to
                                                                                                                                                                                                                                                                                                                   STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                        1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                      GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human death domain containing receptor (DR6) protein-related protein.
                                                                                                                                  Gaps
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                                                                                                          DB 5; Length 330;
                                                                                                                                 4; Indels
                                                                                                                      Pred. No. 2e-122; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   OCGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                         Score 1729;
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                                                                                                        98.0%;
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                                                                                                                                 Matches 323; Conservative
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                                                                                                                      Similarity
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                                                                                    Sequence 330 AA;
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mediated condition or a Thi cell mediated condition in a mammal. The mediated condition or a Thi cell mediated condition in a mammal. The mediated condition comprising a death domain containing receptor (DR6) agonist composition comprising a death domain containing receptor (DR6) agonist condition or a Th2 cell mediated condition in a mammal. A DR6 agonist is useful in the manufacture of a medicament for treating or preventing at Teal. The mediated condition in a mammal. A DR6 agonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with aberrant apoptosis, graft versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy, inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-control activation and activation activation and activation and activation and activation activation and activation and activation and activation and activation activation and activation and activation activation activation activation activation activation and activation activation and activation ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                   or multiple sclerosis in mammal, comprises administering composition comprising death domain containing receptor, DR6 agonist or antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
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                                                                                                                                                                                                                                                 The invention relates to a method for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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Local Similarity 97.9%; Pred. No. 2e-1
nes 323; Conservative 3; Mismatches
                                                                                                                                                                      Disclosure; Page 132-133; 133pp; English
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ABB81641;

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Human IgG gamma 1 heavy chain SEQ ID NO:15.
(first entry)
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25-SEP-2002
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The present invention describes an isolated human zcytor19 protein (I),
and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
antidiabetic, antiatrhritic, neuroprotective, antiinflammatory,
antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic
activities, and can be used in vaccines. (I) or an antibody binding (I)
can be used for suppressing the immune system for reducing rejection of
tissue or organ transplants and grafts and for treating T-cell specific
cleakaemias or lymphomas and autoimmune diseases including rheumatoid
archritis, multiple sclerosis, diabetes mellitus, inflammatory bowel
disease and Crohn's disease. The antibodies can also be used for treating
immunologic renal diseases, glomerulonephritis, mesangioproliferative
climunologic renal diseases, glomerulonephritis, scleroderma, HIV-related
disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the
antibodies can also be used for renal or urological neoplasms and
cliebeases, amyloidosis and haemolytic uraemic syndrome. (I) and the
antibodies can also be used for renal or urological neoplasms and
cliebeases. Human zcytor19 is located to chromosome 1, more specifically to
chromosome 1p36.11. The present sequence represents a human Igg gamma 1
control of the present sequence represents a human igg gamma is
control of the present sequence represents a human igg gamma is
control of the present sequence represents a human igg gamma is
                                                                                                                                                                     Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic; antithematory; antithematic; antitation; neuroprotective; antiinflammatory; antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic; vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus; autoimmune disease; rheumatorid srthritis; multiple sclerosis; HIV; diabetes mellitue; inflammatory bowel disease; Crohn's disease; asthma; immunologic renal disease; glomerulomephritis; vasculitis; polyarteritis; mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis; secondary glomerulomephritis; scleroderma; amyloidosis; multiple myeloma; haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Zyctor19 polypeptides and polynucleotides useful for stimulating immune responses in animals for producing antibodies, and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grant FJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases, leukemia and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 171-172; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novak JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2000; 2000US-0253561P. 07-FEB-2001; 2001US-0267211P.
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                                                                                                 PSVPLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
                                                                                                                                                                                                            300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zcytor17; chromosome 5; 5ql1; cytokine receptor; immunomodulatory; antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic; anscilar; lymphoid; immune; inflammatory; pplennic; blood; bone; infection; immunosuppresame; cytotoxicity; pplennic; blood; bone; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polynucleotide encoding a cytokine receptor zyctor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders.
                    GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                         STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                            LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
                                                                    PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                          STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                    QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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29-JUN-2000; 2000US-0214955P.
08-FEB-2001; 2001US-0267963P.
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N-PSDB; ABA93797.
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5; Length 330; 4; Indels

Score 1729; DB 5; Pred. No. 2e-122; 3; Mismatches 4

Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTPPAVLQSS 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS

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15-JUN-2001; 2001US-0298710P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; fusion protein; IgE Fcepsilon; IgG Fcgamma; FcepsilonRI; allergy; FcepsilonRII; FcgammaRIIB; protein therapy; IgE; IgG; asthma; hay fever; allergic asthma; allergic rhinitis; hay fever; food allergy; atopic dermatitis; drug allergy; peanut allergen.
              for
                                                      S
                                                                                                                                                                                                                                                     121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                      infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful freating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 tc ABA93443 and ABB05730 to ABAB05745 represent sequences used in the exemplification of the present invention
                                                                                                                                                                   1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                            GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                         PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                                                                                                                                                                  STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                              STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDE
                                                                                                                                                        1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                      Gaps
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                                                                                                                  5; Length 330;
                                                                                                                                     Indels
                                                                                                                Score 1729; DB 5;
Pred. No. 2e-122;
3; Mismatches 4
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/label= Hinge_region
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|abel= CH1 region
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/label= CH3_region
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                                                                                                                                     3;
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                                                                                                                 98.0%;
llarity 97.9%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IgG1 Fcgamma region.
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/label= CH
                                                                                                                          Local Similarity
ses 323; Conserv
                                                                                              Sequence 330 AA;
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The invention relates to a novel fusion protein comprising an IgE Prepsilon fragment and an IgG Fcgamma fragment, which binds to an Fcepsilon fragment and an IgG Fcgamma fragment, which binds to an Ecpsilon and an Fcgammas. The fusion protein of the invention may have a use in protein therapy. The fusion protein is useful in treating or preventing IgE-mediated allergies and asthma, such as allergic asthma, allergic rhinitis, hay fever, food allergy, atopic dermatitis and drug allergy. The allergic response is particularly caused by peanut allergen. The present sequence represents the human IgG1 Fcgamma fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                                                                                                        New fusion protein which binds to FcepsilonRI or RII receptor and FcgammaRIIB receptor, useful for treating or preventing allergies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1729; DB 6; Length 330;
Pred. No. 2e-122;
3; Mismatches 4; Indels (
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                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 5; 32pp; English.
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                                                                                                                          WPI; 2003-167440/16
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(TANO-) TANOX INC.
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Reducing the immunogenicity of a fusion protein by changing an amino acid within the junction region spanning a fusion junction of a fusion protein to reduce the ability of the candidate T-cell epitope to interact with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method of reducing the immunogenicity of a fusion protein. The method involves identifying a candidate T-cell epitope within a junction region spanning a fusion junction of a fusion protein and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell proteins for use in therapy. The present sequence is human ammunoglobulin (I [IgG1] heavy chain Fc region. This sequence is used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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3; Mismatches
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Matches 323; Conservative
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method of the invention
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    Homo sapiens.
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                                                                                    (LEXI-) LEXIGEN PHARM
                                                                                                                                                                         WPI; 2003-103259/09.
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given in the exemplification of the present invention

Sequence 330 AA;

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Human, DR6, B-cell mediated disease; immunosuppressive; antirheumatic; antiarthritic; antiasthmatic; dermatological; antinflammatory; antipsoriatic; antidiabetic; cytostatic; neuroprotective; thyromimetic; antithyroid; nephrotropic; antimifertility; vasotropic; virucide; hepatotropic; antibacterial; antiulcer; haemostatic; antianaemic; antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.

Homo sapiens.

WO2003051290-A2.

26-JUN-2003.

10-DEC-2002; 2002WO-US037596

17-DEC-2001; 2001US-0342632P

(ELIL ) LILLY & CO ELI

Liu J, Na S, Song HY, Yang D;

WPI; 2003-541604/51.

Treating or preventing a B cell mediated condition e.g., chronic hepatitis or chronic cirrhosis, in a mammal by administering a pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to the mammal.

Disclosure; Page 96-97; 97pp; English.

The present invention describes a method (MI) for treating or preventing as 0 call mediated condition in a mammal by administering a pharmaceutical composition comprising a DRE aganist or DRE antagonist to the mammal.

Composition comprising B DRE aganist or DRE antagonist to the mammal. By administering a pharmaceutical composition comprising at least one DRE aganist or DRE aganist or DRE aganist or DRE aganist in the manufacture of a medicament for treating or preventing at least one symptom associated with conditions (CI) such as aberrant apportosis, graft-versus-host disease (GVHD), atopy. Theumacolist, multiple ofelerosis, Mahimoto's thyroiditis, Graves disease, transplant rejection, systemic lupus erythemacosus, Behcef's disease, transplant scardiopathy, autoimmune heaptigus, dispathic interstitial, phenomonia, hypersensificity pneumonitis, autoimmune desactis, dispathic interstitis, chronic cirrhosis, flibrosing lung disease, fullminant viral hepatitis, chronic hepatitis, chronic cirrhosis, flibrosing lung disease, fullminant viral hepatitis, chronic cirrhosis, myelodysplasia, multiple organ dysfunction syndrome (MNS), adult to respirate anticipate associated with conditions (C2) such as aberrant apoptors, immunodeficiators of medicament for treating or preventing at least one symptom associated with conditions (C2) such as aberrant apoptors, immunodeficiators of medicament for treating can be part in the manufacture of a medicament for treating can be part in the manufacture of a medicament for treating contition or symptom cell infection, complications (C2) such as a least one condition or

ö The invention provides human antibodies that bind to stem cell factor (SCF) protein. SCF is also known as mast cell growth factor, steel factor or c-kit ligand. Antibodies of the invention are useful for preparing compositions for treating asthma. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain constant region 180 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLXSKLTVDKSRW 300 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180 9 Human, antibody, stem cell factor; mast cell growth factor; asthma; SCF; steel factor; c-kit ligand; gene therapy; heavy chain. GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW STYRVVSVLTVLHQNWANGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE GapB stem cell factor protein, ö Length 330; 4; Indels treating asthma Human A2-G8 SCF antibody heavy chain constant region. ; 9 Pred. No. 2e-122; В OCCINVESCSVMHEALHNHYOORSLSLSPGK 330 301 QQGNVFSCSWHEALHNHYTQKSLSLSFGK 330 3; Mismatches t C Score 1729; New purified human antibody that binds useful for preparing a composition for Example 10; Page 47-48; 94pp; English. Tomkinson A, Neben S; Š AAO31102 standard; protein; 330 16-DEC-2002; 2002WO-US040227. 17-DEC-2001; 2001US-0342174P. 98.0%; (first entry) Conservative WPI; 2003-523500/49. Query Match Best Local Similarity (FARB ) BAYER CORP N-PSDB; AAL62618 WO2003051311-A2. Homo sapiens. Takeuchi T, 06-OCT-2003 26-JUN-2003 Matches 323; 61 121 121 181 AA031102; 181 241 301 RESULT 12 AA031102 셤 g ò 엄 ð 셤 ઠ ઠે 셤 ઠે 셤

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antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, inflammatory diseorders, atherosclerosis, endometriosis, incoplastic disease, bone-related disease, or psoriasis) in a mammal. The present sequence represents a human IgG1 constant region of an anti-Ang-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                                                                                        GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                         6; Length 330;
                                                                                                                                                                                                       Score 1729; DB 6; Length 3
Pred. No. 2e-122;
3; Mismatches 4; Indels
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2002US-0371966P.
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Best Local Similarity 97.9%;
Matches 323; Conservative
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                                                                                                                                                                       Sequence 330 AA;
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12-APR-2002;
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                                                                                                                                      antibody
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                                                                                                                                                                                       GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                         GLYSLSSVVTVPSSSLGTQTYICNVMHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                  1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                    STYRVVSVLTVLHONWMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE
                                                                                      Gaps
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                                                   Score 1729; DB 6; Length 330;
Pred. No. 2e-122;
3; Mismatches 4; Indels
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                                                 Match 98.0%;
Local Similarity 97.9%;
les 323; Conservative 3
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                   Sequence 330 AA;
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N-PSDB; ADF11388
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                                         The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion protein comprises a non-interleukin-2 (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is human immunoglobulin gamma (IgG) constant region. This sequence is used to illustrate the method of the invention
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                                                                                                                                                                                       Gaps
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                                                                                                                                                                                       ;
                                                                                                                                                                 6; Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.
                                                                                                                                                                                      4; Indels
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                                                                                                                                                                Score 1729; DB 6;
Pred. No. 2e-122;
3; Mismatches
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                     Page 51-53; 71pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF11389 standard; protein; 330 AA
 or immune disorders
                                                                                                                                                                98.0%;
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Best Local Similarity 97.9
Matches 323; Conservative
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                                                                                                                                             Sequence 330 AA;
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                      Example 1;
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The present invention describes an isolated human antibody (I) that specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of (I); (2) methods of treating an osteopenic disorder in a patient, comprising administering to a patient the pharmaceutical composition of (I) or a pharmaceutical amount of (I); and (3) a method composition of (I) or a pharmaceutical amount of (I); and (3) a method composition of (I) and phological sample, comprising contacting the sample, to OPGL, and measuring the level of bound antibody in the sample. (I) has osteopathic, antiarthritic and cytosteatic activities, and can be used in treating bone disorders, such as osteoporosis, bone loss from arthritis, pager's disease or osteopenia. The antibody (I) may also be used for detecting OPGL in biological samples and in identifying cells or tissues that produce the protein. The present sequence represent a sequence which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
New isolated antibody that specifically binds osteoprotegerin ligand, useful for diagnosing or treating bone disorders, such as osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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Pred. No. 2e-122;
3; Mismatches 4; Indels
                                      useful for diagnosing or treating bone disorders, such a
bone loss from arthritis, Paget's disease or osteopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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ne : 220.58 secs
                                                                                                                                          Example 3; SEQ ID NO 2; 156pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 330 AA;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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, 2006, 21:31:15 ; Search time 33.6269 Seconds	(without alignments)	944.229 Million cell updates/sec
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February 22,		
Run on:		

US-10-000-439-2	e: 1764	1 ASTROPSVEDIADSSKSTSG
Title:	Perfect score: 1764	Segmence

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* pir4:\* PIR 80:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			SOUTHER	
Result No.	Score	Query	Query Match Length	DB	ID	Description
				Н		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
-	1729	98.0		ч	GHHU	
7	1592.5	90.3		N	A23511	-
m	1590.5	90.5		~	A60764	
4	1566	88.8		Н	G2HU	gamma-2
S	1552.5	88.0		-	G4HU	
9	1225.5	69.5	374	~	869339	Ig heavy chain V r
7	1225	69.4	328	7	147159	
œ	1222	69.3	255	4	S31866	
6	1219	69.1	328	7	147160	
10	1216	68.9	234	~	PT0207	gamma
11	1193	67.6	328	~	147158	
12	1192.5	67.6	323	П	GHRB	_
13	1189	67.4	328	~	147161	
14	1174.5	9.99	329	ч	G2GP	gamma
15	1163.5	99	472	~	S31459	gamma-
16	1144.5	64.9	470	~	S22080	heavy
17	1125.5	63.8		~	C30554	g heavy
18	1123	63.7		Н	G3HUWI	
19	1117.5	63.4	333	~	PS0018	Ig gamma-2b chain
	1116	63.3		7	PC4436	_
21	1114	63.2		7	PS0017	Ig gamma-1 chain C
22	1109	62.9		٦	G1MS	
23	1108	62.8		-	G3MSC	
24	1104	62.6		-	G1MSM	Ig gamma-1 chain C
25	1097	62.2		Н	G3MSM	
26	1093	62.0		ч	G2MSA	gamma-2a
27	1093	62.0	46	7	S37483	
28	1090.5	61.8	335	н	G2MSAB	Ig gamma-2a chain
59	1088	61.7	399	Н	G2MSAM	

Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma 4 chain c	Ig gamma heavy cha	Ig epsilon chain C	Ig heavy chain VHI	Ig heavy chain V-I	Ig heavy chain pre	Ig gamma-1 chain C	Ig gamma-1 heavy c	Ig heavy chain (DO
S00847	S40295	PS0019	806611	G2MSBM	801321	G2MS11	147162	146732	S38864	S69340	A36040	S04845	S14236	A49444	869131
7	~	N	N	٦	7	٦	~	7	~	~	~	~	N	N	~
329	446	322	327	405	475	474	277	180	548	249	218	549	152	220	241
61.5	61.1	6.09	60.3	59.8	58.9	58.8	58.3	37.9	36.8	31.1	31.0	31.0	30.7	30.3	30.2
1085.5	1078	1074	1063.5	1054	1039	1036.5	1028	699	648.5	549	547	547	542	534	532
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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		chain
ULT 1	_	gamma-1
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Grands - Chain C region - human C Species House application 18-Aug-1882 #text\_change 09-Jul-2004 C Jaces in-dam-1981 #sequence revision 18-Aug-1882 #text\_change 09-Jul-2004 C Jaces in-dam-1981 #sequence revision 18-Aug-1882 #text\_change 09-Jul-2004 C Jaces in-dam-1981 #sequence revision 18-Aug-1882 # A02146 C Jacession, J W.; Bergence no mubber: A071-4079, 1982 # A071-4

A;Accession: A590564
A;Molecule type: protein
A;Residues: 136-154, Q', 156-165, Q', 176-176, Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240
A;Residues: 136-154, Q', 156-165, Q', 156-176, Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240
A;Cross-references: UNIPARC: UPI000017378E
A;Note: this sequence has the Gim(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.

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C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A: Fort, b.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c:A;Residues: A23511
A;Molecule type: DNA
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLH 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK 253
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CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiAccession: A60764
RiHuck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobuiin IGHG3 allele (Gmb0, bl, c3, c5, u) with an 3 A;Title: A human immunoglobuiin IGHG3 allele A;Status: A60764
A;Status: preliminary
A;Nolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 80.1%; Pred. No. 4.8e-104; nes 302; Conservative 13; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%; Score 1592.5;
                           301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                         A;Accession: Byle68
A;Molecule type: protein Nie
A;Accession: Byle68
A;Molecule type: protein
A;Accession: Byle68
A;Molecule type: protein
A;Accession: Byle68
A;Molecule type: protein
A;Cross-references: UNIPARC:UP1000017378F
A;Cross-references: UNIPARC:UP1000017378F
A;Note: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W. E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723

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A; Introns: 99/1; 114/1; 224/1
C; Complex: An immunoglobulin hererotetramer subunit consists of two identical light (kap cycomplex: An immunoglobulin hererotetramer subunit sassociate into la c; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology < IM2>
F; 21-35/Domain: immunoglobulin homology < IM2>
F; 23-310/Domain: immunoglobulin homology < IM3>
F; 27-33, 144-204, 250-308/Disulfide bonds: #status experimental
F; 103/Disulfide bonds: interchain (to light chain) #status experimental
F; 109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
ppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)
Jen Primaerstruktur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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                                                                                                                                          A, Reference number: A91668; MUID:77070269; PMID:826475
A, Contents: myeloma protein Nie
A, Accession: B91668
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A;Cross-references: GDB:120085; OMIM:147100
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                                       Hoppe-Seyler's Z. Physiol.
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R.Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Map position: 14932.33-14932.33
C; Complex: An immunoglobulin hererotetramer gubunit consists of two identical light (kai hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l. C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Superfamily: immunoglobulin homology < LML>
E; 20.0-8; Domain: immunoglobulin homology < LML>
E; 20.5; Domain: immunoglobulin homology < LML>
E; 213-202/Domain: immunoglobulin homology < LML>
E; 214/Disulfide bonds: interchain (to light chain) #status experimental
E; 27-83; 140-200, 246-304/Disulfide bonds: #status experimental
E; 210.103; 106, 109; Disulfide bonds: interchain (to heavy chain) #status experimental
E; 27-83; 105-103; 106, 109; Disulfide bonds: interchain (to heavy chain) #status experimental
E; 105, 103, 106, 109; Disulfide bonds: interchain (to heavy chain) #status experimental
E; 105, 108, 108, 108, 109; Disulfide bonds: interchain (to heavy chain) #status experimental
                       R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A;Reference number: A93132; MUD:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A;Title: Disublibide bridges of the heavy chain of human immunoglobulin (A;Teference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
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89.1%; Pred. No. 2.8e-102;
tive 15; Mismatches 17;
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A;Cross-references: GDB:119338; OMIM:147110
                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 238-275 <HOF>
A;Cross-references: UNIPARC:UPI0000173794
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Matches 294; Conservative
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R.Bilison, J.; Hood, J.; Hood, L.
R.Bilison, Linkage and sequence homology of two human immunoglobulin gamma heavy chain cor A; Reference number: A39306; MUD:82197621; PMID:8804948
A; Reference number: A39306; MUD:82197621; PMID:8804948
A; Residues: 1-326 cELL-
A; Cross-references: UNIPROT:PD1859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:932
A; Residues: 1-326 cELL-
A; Cross-references: UNIPROT:PD1859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:932
A; Reference number: A92809 will:B1007873; PMID:6774012
A; Mote: Lys-326 is probably removed posttranslationally
R; Wang, A.C.; Tung, E.; Fudenberg H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fA; Reference number: A92809 will:B1007873; PMID:6774012
A; Contentis: myeloma protein Til
A; Residues: 1-19, 'Q', 21-57, 'Z', 'S9,'A', '61-193,'D', 195-325 cWAN>
A; Cross-references: UNIPARC:UPI00001377; PMID:113060
A; Title: The amino acid sequences of the three heavy chain constant region domains of a A; Reference number: A90752; MID:80001357; PMID:113060
A; Contents: myeloma protein Zie
A; Accession: A90752; MID:80001357; PMID:113060
A; Contents: myeloma protein Zie
A; Residues: 1-24, 'E', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', '199-A; Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMI SRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNVKIKPREEQYNSIYRVVSVLIVLH 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 QNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK 253
                                                                                                                                                                                                                                                                                                               1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
                                                                                                                                                                                                                                                                                                                                                                                              86 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------BPKSCDKTHTCPPCPAPELLGGPSVFLPPPKPKDT
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                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                      47;
                                                                                                                                                              Length 377;
                                                                                                                                                                                                                      Indels
                       ;Cross.references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B;Superfamily: immunoglobulin homology;Keywords: immunoglobulin;to-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                              61 GLYSLSSWYTVPSSSLGTQTYICNVNHKPSNTKVDKKV----
                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                      15;
                                                                                                                                                           Ouery Match 90.2%; Score 1590.5; DB 2, Best Local Similarity 80.1%; Pred. No. 6.6e-104; Matches 302; Conservative 13; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 ALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||| : |:||||||||
361 ALHNRFTQKSLSLSPGK 377
Residues: 1-377 <HUC>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRMP
A;Residues: 1.328 «KAC»
A;Cross-references: UNIPARC:UPIO000115524; EMBL:U03779; NID:g433123; PIDN:AAA52217.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iggamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158; MUID:95015845; PMID:7930579
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A;Reference number: S69339; MUID:95262687; PMID:7744049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSVGSFFLYSKLIVDKSRWQQGNVF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQRNVF 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 TQTYICNVN-----HK-PSNTKVDKKVBPKSCDKTHTCPPCPAPELLGGPSVFLF
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.5%; Score 1225.5; DB 2; Length Best Local Similarity 87.1%; Pred. No. 2.2e-78; Matches 230; Conservative 6; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Reddues: 1-140, CC', 142-374 <KH2>
A;Coss-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin]
                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Reference number: S72664
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                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
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Matches 224;
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A; Map position: 1493-33-494932.33
A; Map position: 1493-33-494932.33
A; Map position: 1493-33-494932.33
A; Map position: 1493-33-494932.33
A; Introns: 99/1; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as 19A and 19M, the subunits associate into 1; S; Seywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IM1>
F; 34-203/Domain: immunoglobulin homology <IM2>
F; 240-307/Domain: immunoglobulin homology <IM3>
                                                                                                                                                                                                                                                                                                                                                                                                                            constant
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C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/John immunoglobulin homology <IM3>
F;240-307/John immunoglobulin homology <IM3>
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted
                g gamma-4 chain C region - human
Species: Homo sapiens (man)
Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
Accession: A90933; A90249; A02150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                  R/Elison, J.: Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/TILle: Nucleotide sequence of a human immunoglobulin C-gamma4 gene
A/Reference number: A90933; MUID:83157104; PMID:6299662
A/Accession: A90933
A/Molecule type: DNA
A/Residues: 1-327 < ELL>
A/COSS-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A/Note: the sequence was determined from the germline gene
R/PINK, J. R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Blochem. J. 117, 33-47, 1970
A/Title: Human immunoglobulin sublclasses. Partial amino acid sequence number: A90249; MUID:70207560; PMID:4192699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.0%; Score 1552.5; DB 1; Length 327; 88.8%; Pred. No. 2.5e-101; ive 15; Mismatches 19; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A90249
A;Molecule type: protein
A;Realdues: 1-30;81-326 <PIN>
A;Cessidues: 1-30;81-326 <PIN>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Matches 293;
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A;Residues: 1-328 «KAC>
A;Residues: 1-328 «KAC>
A;Cross-references: UNIPARC:UP1000115525; EMBL:U03780; NID:g433125; PIDN:AAA52218.1; P
A;Genetias: 1g62b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology < IMM>
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[Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Dave-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 < ERR>
A;Cross-references: UNIPARC:UP10000176F05
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                      ; Score 1219; DB 2;
; Pred. No. 5.2e-78;
45; Mismatches 58;
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Pred. No. 5.5e-78;
4; Mismatches 6;
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Best Local Similarity 67.2%;
Matches 223; Conservative 4:
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Best Local Similarity 95.7%;
Matches 224; Conservative
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 14716
C;Accession: 14716
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences (A;Reference number: 147188; MUID:95015845; PMID:7930579
A;Reference number: 147188 MUID:95015845; PMID:7930579
A;Status: preliminary; translated from GB/EMBL/DDBJ
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GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                             PSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                       LIKNOVSLICLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGSFFLYSKLTVDKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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A; Residues: 1-47,'E',49-71,'PV',72-128 A; Residues: 1-47,'E',49-71,'PV',72-128 A; Gross-references: UNIPARC: UP00001737B
R; Wartens C.L.; Moore, K.W.; Steinmer, M.; Hood, L.; Knight, K.L.
R; Wartens C.L.; Moore, K.W.; Steinmer, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A; Milte: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain section number: A39328
A; Molecule type: mANA
A; Residues: 88-103, Wi, 105-143, E', 1845-184, A', 186, 'E', 188-266 <MAR>
A; Residues: B8-103, Wi, 105-143, E', 145-184, A', 186, 'E', 188-266 <MAR>
A; Residues: B8-103, Wi, 105-143, E', Nole, L.E.; Porter, R.R.
A; R; Fruchter, R.G.; Jacken, S.A.; Mole, L.E.; Porter, R.R.
A; R; Fruchter, R.G.; Jacken, S.A.; Mole, L.E.; Porter, R.R.
A; R; Fruchter, R.G.; Jacken, S.A.; Mole, L.E.; Porter, R.R.
A; R; Fruchter, R.G.; Jacken, S.A.; Mole, L.E.; Delaney, R.R.
A; R; Fruchter, R.G.; And R; R; Fallows Jr., R.E.; Delaney, R.
A; Residues: 132-143, E', 145-161 
A; R; Fruchter, R.G.; And R; R; Fallows Jr., R.E.; Delaney, R.
A; Residues: 132-143, E', 145-161 
A; R; Fruchter, R.G.; And R; R; Fallows Jr., R.E.; Delaney, R.
A; Residues: 129-13; 1155-172, D', 174-184, A', 186, E', 188-200, D', 202-217, E', 219-232, Q', A; Residues: 129-13; 1155-172, D', 174-184, A', 186, E', 188-200, D', 202-217, E', 219-232, Q', A; Residues: 129-13; 1155-172, D', 174-184, A', 186, E', 188-200, D', 202-217, E', 219-232, Q', A; Residues: 129-13; 1155-172, D', 174-184, A', 186, E', 188-200, D', 202-217, E', 219-232, Q', A; Residues: 129-13; 1155-172, D', 174-184, A', 186, E', 188-200, D', 202-217, E', 219-232, Q', A; Residues: 129-13; 1155-172, D', 174-184, A', 186, E', 188-200, D', 202-217, E', 219-232, Q', A; Residues: 129-13; 1155-172, D', 174-184, A', 186, E', 188-200, D', 202-217, E', 219-232, C', A; Residues: 129-13; 1155-172, D', 174-184, A', 186, E', 188-200, D', 202-217, E', 219-232, D', 174-184, A', 186, E', 
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147161
Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLEPPKEKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 323;
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Matches 222; Conservative
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C;Species: Oryctolagus cuniculus (Gomestic rabbit)
C;Species: 24-Apr-1994 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C;Date: 24-Apr-1994 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C;Date: 24-Apr-1994 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C;Date: 24-Apr-1995 #99289; A90245; A94416; A02161
R;Bernetein; K.E.; Alexander; C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot A;Reference number: A91749; MUID:84030930; PMID:6313520
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Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A;Reference number: A90290; MUID:76135469; PMID:1243651
A;Accession: A90290
A;Molecule type: protein
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A;Residues: 1-323 <BER>
A;Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A;Orte: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M; Mole, L.E.
Biochem. J. 151, 337-349, 1975
                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:9433121; PIDN:AAA52216.1;
                                                                                                                                                                                                                                                                                                                      οĘ
                                                                                                                                                 ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 147158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the CDNA sequences A;Reference number: 147158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 STYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAAEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                   234
                   PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.6%; Score 1193; DB 2; Best Local Similarity 67.2%; Pred. No. 3.4e-76; Matches 223; Conservative 42; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-328 «KAC>
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C.Species: Cavia porcellus (guinea pig)
R.Firischmann. T.M.
submitted to the Alas, April 1975
A.Reference number: A94553
A.Accession: A90352; MUD:71058471; PMID:5538606
A.Accession: A90352; MUD:71058471; PMID:5538606
A.Accession: A90352
A.Accession: A90353
A.Accession: A90353
A.Accession: A90359
A.Accession: A9059, MUD:71058486; PMID:5538616
A.Accession: A9059, MUD:71050001737A0; WIPPARC:UPIO0001737A1
A.Fitle: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami
A.Residues: 69-13; 312-339
A.Accession: A90359
A.Accession: A9059, MUD:71050001737A0; WIPPARC:UPIO0001737A1
A.Fitle: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami
A.Residues: 69-13; 312-339
A.Accession: A9054003
A.Accession: A9054003
A.Accession: A9054003
A.Accession: A9054003
A.Accession: A9054003
A.Accession: A9054003
A.Accession: A7054003
                                                                                      A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 «KAC>
A;Residues: 1-328 «KAC>
C;Crose-references: UNIPARC:UPI0000115526; EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PI
C;Genetics:
A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology < IMM>
                   ಹ
A,Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A,Reference number: I47158; MUID:95015845; PMID:7930579
A,Accession: I47161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::::|::|||| |||| ||| ||| ||| ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ISRSKVIVICLVIGFYPPDIHVEWKSNGQPEPEGNYRTIPPQQDDGTFFLYSKLAVDKA 296
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9
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A;Cross-references: UNIPARC:UP10001737A2

R;Trischmann, T.M.; Cebra, J.J.

Biochemistry 13, 4804-4811, 1974

A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.

A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90385; MUID:75036073; PMID:4609467

A;Residues: 227-311 - CTR2.

A;Residues: 227-311 - CTR2.

A;Cross-references: UNIPARC:UP100001737A3

B;Odiveira, B.; Lamm, M.E.

Biochemistry 10, 26-31, 1971

A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A;Reference number: A9034; MUID:71058474; PMID:4922544

A;Cross-reference number: A9034; MUID:71058474; PMID:4922544

A;Cross-reference number: A9034; MUID:71058474; PMID:4922544

A;Crost-ente: annotation; disulfide bonds

A;Note: Cys-16; Is involved in a heavy-light chain bond

A;Note: Cys-16; Is involved in a heavy-light chain bond

A;Note: Cys-16; Is involved in a heavy-light chain bond

A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds

A;Note: Cys-10; Cys-107, and Cys-110 form inter-heavy chain bonds

A;Note: Cys-10; Is involved in a heavy-light chain bond

A;Note: Cys-10; Jys-10; and Cys-110 form inter-heavy chain bonds

C;Complex: An immunoglobulin hear-ote-tramer subunit consists of two identical light (kan hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into 1 C;Superfamily: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;241-30/Domain: immunoglobulin homology <IM3>
F;241-202/Disulfide bonds: #status experimental

F;178-202/Disulfide bonds: #status experimental

F;248-308/Disulfide bonds: #status experimental
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$31459
Ig gammal chain - sheep (fragment)
Ig gammal chain - sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
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C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ar
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A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
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E
                                                                                  Query Match 66.0%; Score 1163.5; DB 2; Length 472; Best Local Similarity 65.7%; Pred. No. 6.3e-74; Matches 218; Conservative 40; Mismatches 71; Indels 3;
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Residues: 1-472 <PAT>
A;Cross-references: UNIPARC:UPI0000176F35; EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>
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Search completed: February 22, 2006, 21:38:16 Job time : 34.6269 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

February 22, 2006, 21:24:24; Search time 219.43 Seconds (without alignments) 1061.041 Million cell updates/sec Run on:

US-10-000-439-2 1764 1 ASTKGPSVPPLAPSSKSTSG.......MHEALHNHYQQRSLSLSPGK 330 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 Total number of hits satisfying chosen parameters: 2166443 seqs, 705528306 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

SUMMARIES

			sapien	sapien	sapien	sapien	sapien	sapien	sapien		sapien	sapien	sapien	sapien		sapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	bygma	sapien		sapien	sapien	sapien	sapien	sapien
tion	homod	homo	homo	homo	homo	рошо	homo	рошо	homo	homo	рошо	рошо	homo	рошо	рошо	homo	рошо	homo	ношо	рошо	homo	рошо	homo	pongo	рошо	homo	homod	рошо	рошо	homo	homo
Description	P01857	Q6gmx6	Q569f4	0727p5	07z5w1	Q6pja4	Q5efe5	Q6gmw7	Q6gmx1	Q6in78	Q6n089	Q6p055	Q6mzq6	Q6n094	Q6n097	Q7z351	060U9G	Q6pyx1	Q6pi81	Q6pjf1	Q60095	Q6pj95	Q6mzv7	Q5re17	Q6n030	Q5ebm2	Q8n4y9	Qenf17	P01859	Q6n093	Q6p6c4
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& Query Match	98.0	98.0	98.0	98.0	98.0	98.0	98.0		98.0	97.8	97.8	۲.	97.8	97.8	97.8	•	97.6		97.5	97.5	97.4	7.	96.9	4.	ö	90.3	90.1	89.4	88.8	88.8	88.5
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P01861 homo sapien Q8tc63 homo sapien Q68cn4 homo sapien Q6mzu6 homo sapien Q6mzu7 homo sapien Q8ctt2 homo sapien Q95m34 equus cabal Q95m34 equus cabal Q65z12 mus sp. fv/ P01870 oryctolagus P01862 cavia porce P01861 rattus norv Q5m839 rattus norv	
IGHG4 HUMAN 068TC63 HUMAN 068CM4 HUMAN 06MXZ1 HUMAN 06MXZ7 HUMAN 06MXZ7 HUMAN 065TZ2 HUMAN 055CQ8 HUMAN 055CQ8 HUMAN 05CQ8 TZ2 HUMAN 06CR RABIT IGHG3 CAVPO IGHG3 HUMAN GCB RAT 05M839 RAT	
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UUUUUUUUU 44444 UU 4 U O C O C C C C C C C C C C C C C C C C	

## ALIGNMENTS

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1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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                                                                                                                          K -> R (in GlM(3) marker).
/FIId=VAR 003886.
D -> E (in GlM(non-1) marker).
FIId=VAR 003887.
L -> M (in GlM(non-1) marker).
/PIId=VAR_003888.
                                                           Interchain (with light chain).
Interchain (with heavy chain).
Interchain (with heavy chain).
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Hinge.
CH2.
CH3.
N-linked (GlcNAc. . .).
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Pred. No. 6e-119;
3; Mismatches 4;
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Best Local Similarity 97.9
Matches 323; Conservative
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284
296
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 1110
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330 AA;
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DISULFID
VARIANT
                                    CARBOHYD
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                                                                                                                                                                                                                            MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal Ig21 immunoglobulin (upseloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Roppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.
             Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Blochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BR 18 A 94313; GHUU

RR PB; A9313; GHUU

RR PB; A1313; GHUU

RR PB; A1313; GHUU

RR PB; A1313; GHUU

RR PB; A1477; X-ray; H=1-103.

RR PB; DB5; X-ray; H=1-101.

RR PB; DB5; X-ray; H=1-101.

RR PB; DB5; X-ray; H=1-101.

RR PB; DB5; X-ray; A/B=106-326.

RR PB; DB7; X-ray; A/B=106-329.

RR PB; DB7; X-ray; A/B=106-329.

RR PB; DB7; X-ray; A/B=106-329.

RR PB; DB7; X-ray; A/B=107-330.

RR PB9; DC0X; X-ray; A/B=107-330.

RR PB9; DC0X; X-ray; A/B=107-330.

RR PB9; DC0X; X-ray; A/B=107-330.

RR PB9; A17100; A1
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                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE=81208100; PubMed=7236608;
  MEDLINE=71064027; PubMed=4923144;
                                                                            DISULPIDE BONDS
                                                                                                                                                                                                                      Deisenhofer J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    removed.
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Q569F4 HUMAN PRELIMINARY;
Q569F4;
                                                                                                                                            Matches 323; Conservative
     Pfam; PF07654; C1-set; 3.
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                                                                                                                                 Similarity
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                                                                                                                    Query Match
Best Local S:
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TISSUE-Primary B-Cells;

MEDINE-2238825; PubMed-12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heise F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muxny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Hakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schaerch A., Schmutz J.M., Marra M.A.;

Schaerch A., Schini J.E., Jones S.J.W., Marra M.A.;
                                        120
                                                                                          PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                                                                                                                                                                                                 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
                                                                                                                                                                                                           241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
                9
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                     STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                         Submitted (UM)-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC073766; AAH73766.1; -; mRNA. GG, GO.0016021; C:integral to membrane; IEA. InterPro; IPR003599; IG. InterPro; IPR007110; IG-like. InterPro; IPR003597; Ig-c1. InterPro; IPR003597; Ig-c1. InterPro; IPR0030697; Ig-d1. InterPro; IPR0030697; Ig-d1.
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QGGMX6;
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WEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausborg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

RATausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jeden H., Moore T., Max S.I., Wang J., Halen F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

RA Chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzry D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rabakseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ra Bakesley R.W., Touchman J.W., Gremen E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS00359; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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Last annotation update)
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97.9%; Pred. No. 9.3e-119;
ative 3; Mismatches 4;
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QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Q7Z5W1;
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TISSUE-Spleen;

KINCLEOTIDE SEQUENCE.

TISSUE-Spleen;

KINCLEOTIDE SEQUENCE.

KINCLEOTIDE SEQUENCE.

KINCLEOTIDE SEQUENCE.

KINCLEOTIDE SEAL, Grouse L.H., Derge J.G.,

KINCLEOTIDE SEAL, Grouse L.H., Derge J.G.,

KINCLEOTIDE S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Hatch F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RAICHARS S., Worley K.C., Malek J.A., Gunaratne P.H.,

RAICHARS S., Worley K.C., Male S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Ratchard S., Worley K.C., Male S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rackinguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
'Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                      Length 469;
                                                                                                                                                                               Indels
                                                                                              Submitted (ÅPR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092518; AAH92518.1; -; mRNA.
SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                 Query Match 98.0%; Score 1729; DB 2; Best Local Similarity 97.9%; Pred. No. 9.4e-119; Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 OCGNVFSCSVMHEALHNHYOORSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7Z7PS_HUMAN PRELIMINARY;
Q7Z7PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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Name=IGHG1;
                                                                      TISSUE=Lymph;
NIH MGC Proje
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 PSVFLEPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGYN
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 469;
                                                                                                                                                                                                              TISSUE-Spleen;

NUM MGC Project;

Submitted (Paroject)

Submitted (Paroject)

EMBL; BC051228; AAH51328.1; -; mRNA.

HSSP; P01857; 1H731.

SMR; Q727P5; 20-469.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR003596; Ig-MrC.

InterPro; IPR003596; Ig-MrC.

InterPro; IPR003596; Ig-W.

Emm; PF07654; C1-8et; 3.

SMART; SM00406; IG-W.

PROSITE; PS00290; IG-MHC; UNKNOWN_2.
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SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 98.0%; Score 1729; DB 2; Best Local Similarity 97.9%; Pred. No. 9.4e-119; Matches 323; Conservative 3; Mismatches 4;
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TISSUB-Primary B-Cells,

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feligodd B.A., Grouse L.H., Derge J.G.,

A Rlauber R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A phykins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisch F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A papleton M., Soares M.B., Bonaddo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Perers G.J., Abramon R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

" "Generation and initial analysis of more than 15,000 full-length human
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             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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TISSUB-Primary B-Cells;
NIH MGC Project;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018747; AAH18747.1; -; mRNA.
HSSP; P01861; 1ADQ.
SMR; QEDJA4; 20-470.
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SWART; SM00407; IGc1; 3.
SWART; SM0406; IGc1; 3.
PROSITE; SM02005; IGV; IIKB; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SEQUENCE 470 AA; 51716 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 9.4e-119;
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3; Mismatches
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_G1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-set; 3.
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Matches 323; Conservative
                                                                                                                  NCBI_TaxID=9606;
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             요. 첫
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B rownstein M.J., Usdin T.B., Toobliyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.J., Hulyk S.W.,

Richards S.W., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley B.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman M., Gren B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Rodriguez A. C., Grimwood J., Schmutz S., Marra M.A.,

Rodriguez A., Schen B.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO53984; AAH53984.1; -; mRNA.
HSSP; P01857; 1HZH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR00110; Ig-like.
InterPro; IPR0013597; Ig_c1.
InterPro; IPR001306; Ig_MHC.
InterPro; IPR001306; Ig_V.
Pfam; PP07654; C1-set; 3.
SMART; SM00406; ICv; 1.
PROSITE; PS500135; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
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Last sequence update)
Last annotation update)
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JA4 HUMAN
QēDJA4 HUMAN PRELIMINARY;
GEBJA4;
GS-JUL-2004 (TREMBLRel. 27, Cx
05-JUL-2004 (TREMBLRel. 27, La
05-JUL-2004 (TREMBLRel. 27, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Spleen;
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Name=IGHG1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVFLFFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                Gaucher C., Klein P., Beliard R.; "Sequence determination of the recombinant human anti-RhD monoclonal antibody T125.";
                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
anti-RhD monoclonal T125 gammal heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.0%; Score 1729; DB 2; Length 475; 97.9%; Pred. No. 9.5e-119; ive 3; Mismatches 4; Indels C
                                                                                                                                                                                                                                                       Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AY89492; AAW82028.1; -; mRNA.
InterPro; IPR00359; Ig.
InterPro; IPR0040396; Ig.
InterPro; IPR0040396; Ig.
InterPro; IPR0040396; Ig.
InterPro; IPR004039; Ig.
InterPro; IPR004039; IG.
InterPro; IPR004039; IG.
InterPro; IPR0040396; IG.
InterPro; IPR0040396; IG.
InterPro; IPR004039; IG.
InterPro; IPR0515; IG.
INTER; IPR00403; IG.
IPR05ITE; IPS004390; IG.MHC; UNKNOWN_2.
                                                                                               10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Anti-RhD monoclonal T125 gammal heavy chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      chain.
1367D400DC7D2859 CRC64;
          QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                          QSEFES HUMAN PRELIMINARY;
QSEFES;
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475
                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                     NCBI_TaxID=9606;
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Astraubberg R.L., Feingold E.A., Crouse L.H., Derge JG., Structure... Incurre... L. Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Riausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altachul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K., Altachul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K., Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rapornstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Rohards S., Wolfley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., R. A., Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schentz J., Where R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schent J., Jones S.J.M., Marra M.A.; and mouse cDNA sequences...; US.A., 99:16899-16903(2002).
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                                                                                                                                         Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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SEQUENCE 475 AA; 51987 MW; 2AlFE55D736860F8 CRC64;
                                                          Created)
Last sequence update)
Last annotation update)
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     475 AA
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        PRT;
                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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Matches 323; Conservative
QGGMW7_HUMAN PRELIMINARY;
QGGMW7;
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IGHG1 protein.
Name=IGHG1;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUSPER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MISCHOLL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHOLL S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Romas S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raden J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radinguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Schlaka U., Smailus D.E.,

B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                   300
                                                                                                  445
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                   LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
                                                                                     386 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC073773; AAH73773.1, -; mRNA. GO; GO:0016021; C:integral to membrane; IEA. InterPro; IPR007399; Ig. InterPro; IPR00710; Ig-11ke. InterPro; IPR003597; Ig_c1. InterPro; IPR003506; Ig_WC. InterPro; IPR003596; Ig_W.
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                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheital protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                  OQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
HYPOCHELICAL Protein_
SEQUENCE 476 AA; 52286 MW; 622AA
                                                                                                                                                                                                                                                      OGGMX1 HUMAN PRELIMINARY;
OGGMX1;
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
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TISSUE=Spleen;
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DB 2; Length 476;

98.0%; Score 1729;

Query Match

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MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausener R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

A bistchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Willano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Redenstein and initial analysis of more than 15,000 full-length human
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                        147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                        267 PSVFLFPPKPXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                     Indels
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TISSUE=Peripheral Nervous System;
NIH MCC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072419; AAH72419.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Pred. No. 9.6e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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97.98;
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QGIN78;
Best Local Similarity 97.99
Matches 323; Conservative
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NUCLEOTIDE SEQUENCE.
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TISSUE=Peripheral Nervous System;

RX Straubberg N. Feingold E.A., Grouse L.H., Derge J.G.,

RBDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RIA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Districtency L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rabia S.S., Logdellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabia S.S., Logdellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                              Gaps
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                                                                                                            Length 472;
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS02909; IG MHC; UNKNOWN_2.
HYPOCHELICAL protein.
SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
[2]
                                                                                                                                                4.
                                                                                                        97.8%; Score 1726; DB 2;
97.6%; Pred. No. 1.6e-118;
ive 4; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGP055 HUMAN PRELIMINARY;
Q6P055;
                                                                                                                             Best Local Similarity 97.6
Matches 322, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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Bukaryota, Metazoa: (bordata; Craniata; Vartebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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A Pobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
EMBL; BX640627; CAE45781.1; -; mRNA.
R HSSP; P01861; 1ADO.
R InterPro; IPR001359; Ig.
R InterPro; IPR003597; Ig.-1.
R InterPro; IPR003506; Ig-MHC.
R InterPro; IPR003506; Ig-MHC.
R InterPro; IPR003506; Ig-WHC.
R InterPro; IPR003506; Ig-WHC.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
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                                                                                                                                                                                                                                       Length 466;
Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686P15220.
Name=DKFZp686P15220.
Homo sapiens (Human).
                                                                                                                                                                                                                                       97.8%; Score 1726; DB 2;
97.6%; Pred. No. 1.5e-118;
iive 4; Mismatches 4;
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The German cDNA Consortium;
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Q6N089;
                                                                                                                                                                                                                                                                             Matches 322; Conservative
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                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 STYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CS-0701-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mypothetical protein DKFZp686001196.
Name=DKFZp686001196;
Homo sapiens (Human)
Eukaryota, Metazoa (Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 PSVFLEPPKFKDTLMISRIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGYN
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C TISSUE=Esophagus tumor;

TISSUE=Esophagus tumor;

TISSUE=Esophagus tumor;

The German Chan M. Ween H.W., Weil B., Amid C., Osanger A.,

A Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

A Fobo G., Han M., Wiemann S.;

ENDL; BX440622; CAE45776.1; -; mRNA.

EMBL; BX640622; CAE45776.1; -; mRNA.

R InterPro; IPR001359; Ig.

R InterPro; IPR001359; Ig.

R InterPro; IPR001306; Ig_MHC.

R InterPro; IPR00306; Ig_MHC.

R InterPro; IPR00359; Ig.

R Pfam; PF07654; Cl-set; 3.
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SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          97.8%; Score 1725; DB 2;
97.6%; Pred. No. 1.9e-118;
iive 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446 QQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475
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                InterPro; IPR007110; Ig-1; interPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003006; Ig_W.
Pfam; PF07654; C1-8et; 3.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 2.
SWART; SW00466; IGW; 1.
PROSITE; PS050835; IG_LIKE; 4.
PROSITE; PS050835; IG_LIKE; 4.
Hynotherical profesion
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Q6N094;
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Matches 322; Conservative
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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TISSUB=Escophagus tumor;
The German consortium;
The German consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BX640947; CAE45972.1; -; mRNA.
HSSP; P01861; 1ADQ.
SMR; Q6MZQ6; 20-475.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                   TISSUE=Peripheral Nervous System;
Strausberg R.;
Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
REMBL; BCG65820; AR465820.1; -; mRNA.
RISP; PO1861; JADQ.
RICEPTO; IPR001369; Ig.
RICEPTO; IPR003597; Ig.cl.
REMBRT; SM00409; IG.y.
REMBRT; SM00409; IG.l.
REMBRT; RESCORSS; IG.LIKE; 4.
REMSTITE; PS00290; IG.MHC; UNKNOWN_2.
REMOSITE; PS00290; IG.MHC; UNKNOWN_2.
REMOSITE; PS00290; IG.MHC; UNKNOWN_2.
REQUENCE 473 AA; 51344 WW; 9816D56A77129B57 CRC64;
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NUCLEOTIDE SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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NCBL TaxID=9606;

N [1]

NUCLEOTIDE SEQUENCE.

TISSUE=Espaphagus tumor;

TISSUE=Espaphagus tumor;

TISSUE=Espaphagus tumor;

THe German cDNA Consortium;

Wamburt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Amburtt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

B. Chob G., Han M., Wiemann S.

E. Mail, Isk40619; CRR45773.1; -; mRNA.

ILLE PROJ 1861; 1ADO.

REMBI; SR003199; IG.

RICEPRO; IPR003109; IG.

RICEPRO; IPR003106; IG_MHC.

REMBI; PROJ 64; CL-set; 3.

RART; SM00409; IG; 2.

RART; SM00406; IGV; 1.

DR SWART; SM00406; IGV; 1.

PROSITE; PS00210; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                  Query Match 97.8%; Score 1725; DB 2; Length 480; Best Local Similarity 97.6%; Pred. No. 1.9e-118; Matches 322; Conservative 3; Mismatches 5; Indels (
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00201 IG_MHC; UNKNOWN_2.
Hypochetical protein.
SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;
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481 AA; 52759 MW; 47220D9E64BDF98B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686H20196.
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Q6N097;
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SEQUENCE 48
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                                                             STYRVUSVLTVLHQNMMGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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   Length 481;
                                Indels
Score 1725; DB 2;
Pred. No. 1.9e-118;
3; Mismatches 5;
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Job time : 222.43 secs
   Query Match
Best Local Similarity 97.6%;
Matches 322; Conservative
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22, Appli 81, Appl 31, Appl 45, Appl 8, Appli 139, App

Sequence Sequence Sequence

Sequence 45, Al Sequence 8, Api Sequence 139,

Sequence Sequence

38, Appli 1, Appli 22, Appl 44, Appl 44, Appl 44, Appl 44, Appl 44, Appl 98, Appl 167, App

Sequence

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Sequence Sequence

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61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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US-09-047-208-2

Sequence 2, Application US/09047200

Publication No. US20030002190A1

GENERAL INFORMATION:

APPLICANT: SAAND, Ke

APPLICANT: Zhang, Ke

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: UGG-MEDIATED ALLERGIC DISEASES

FILE REFRENCE: UGG-002A

CURRENT APPLICATION NUMBER: US/09/041,208

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177

SEQ ID NO 2.

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1764; DB 3;
100.0%; Pred. No. 1.3e-128;
iive 0; Mismatches 0;
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US-10-867-58-2
US-10-867-596-31
US-10-937-596-31
US-10-883-576-45
US-10-883-576-45
US-10-901-736-60
US-10-901-736-60
US-10-901-736-60
US-11-094-555-38
US-11-094-98-22
US-11-090-846-44
US-11-090-846-44
US-11-090-847-44
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  ORGANISM: Homo sapiens
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  330;
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                                                                   February 22, 2006, 21:57:24; Search time 168.705 Seconds
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1 ASTKGPSVFPLAPSSKSTSG......MHEALHNHYQQRSLSLSPGK 330
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Sequence
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-698-907-22
US-10-928-305-7
                                                                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                                                                            1867569 seqs, 417829326 residues
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                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                    Perfect score:
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241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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              Length 330;
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                                                                    4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQUENCE 15, Application US/09995898A

PUblication No. US20030027253A1

GENERAL INFORMATION:
APPLICANT: Preenell, Scott R.
APPLICANT: Wo. US20030027253A1ak, Julia E.
APPLICANT: Mo. US20030027253A1ak, Julia E.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFRENCE: 00-108
CURRENT APPLICATION NUMBER: US/09/995,898A
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR PILING DATE: 2001-01-08

PRIOR FILING DATE: 2001-01-08

PRIOR FILING DATE: 2001-02-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEG for Windows Version 3.0

LENGTH: LENGTH:
              Score 1732; DB 5;
Pred. No. 4e-126;
98.2%; Pred. No. ac. 2; Mismatches
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              Query Match
Best Local Similarity 98.2<sup>3</sup>
Matches 324; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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Sequence 29, Application US/10966673

Publication No. US20052268641

GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Tsurushita, Naoya
FILE REFERENCE: 05882.0039.NAUS07

CURRENT APPLICATION NUMBER: US/10/966,673

CURRENT PRILING DATE: 2004-10-15

PRIOR FILING DATE: 2004-10-15

PRIOR FILING DATE: 2004-04-14

PRIOR FILING DATE: 2004-04-14

PRIOR FILING DATE: 2003-10-15

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PATENTING DATE: 2003-10-15

NUMBER OF SEQ ID NOS: 77

LENGTH: 330
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           US-10-00-439-2

Sequence 2, Application US/10000439

Fublication No. US20030064063A1

GENERAL INFORMATION:

TILLE OF INVENTION: FUSION MOLECULES AND METHODS FOR

TILLE OF INVENTION: TREATMENT OF IMMUNE DISEASES

FILE REPRENCE: UCO67.004A

CURRENT APPLICATION NUMBER: US/10/000,439

CURRENT FILING DATE: 2001-024

PRIOR FILING DATE: 2001-05-01
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                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-10-000-439-2
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CORGANISM: HOMO SAPIENS
US-10-966-673-29
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 330
TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: MYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
FILE REFERENCE: 030905.0004.CIPI
CURRENT APPLICATION NUMBER: 2010-10-26
FRICH APPLICATION NUMBER: PG/1001/13932
FRICH FILING DATE: 2001-04-28
FRICH FILING DATE: 2000-04-28
FRICH FILING DATE: 2000-04-28
FRICH FILING DATE: 2000-04-28
FRICH FOR APPLICATION NUMBER: 60/200,298
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FRICH FOR APPLICATION NOWER: 2.1
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; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT PILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
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Pred. No. 6.8e-126;
3; Mismatches 4;
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Matches 323; Conservative
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CORGANISM: Homo sapiens
US-10-269-805-68
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          241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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                                                                                   LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
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Pred. No. 6.8e-126;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                          Sequence 38, Application US/09892849
Fublication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Waijper, Joseph L.
APPLICANT: Waijper, Joseph L.
APPLICANT: Waijper, Joseph L.
APPLICANT: Wainer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT APPLICATION NUMBER: US 60/214,282
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2010-06-29
NUMBER: PSEC ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 38
INCHEST: Homo sapiens
                                                                                                                                                                               301 QOGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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US-10-047-542-20
; Sequence 20, Application US/10047542
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Best Local Similarity 97.9%;
Matches 323; Conservative 3
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US-09-892-949-38
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Sequence 81, Application US/10320231A
Sequence 81, Application NO US20030194405A1
GENERAL INFORMATION:
APPLICANT: Neben, Steven
APPLICANT: Takeuchi, Toshihiko
APPLICANT: Takeuchi, Adrian
ITILE OF INVENTION: Area ment Of Asthma
TITLE OF INVENTION: Treatment Of Asthma
FILE REPERENCE: 7430*163
CURRENT APPLICATION UNDMER: US/10/320,231A
CURRENT FILING DATE: 2002-12-19
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                                                                                                                                                       Sequence 1, Application US/10112582

Publication No. US20030166877A1

GENERAL INFORMATION:
TITLE OF INTERPRETENCE:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/112,582

CURRENT APPLICATION NUMBER: US/10/112,582

CURRENT FILING DATE: 2002-03-29

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PatentIn version 3.0

LENGTH: 330

TYPE: PRT
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; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.0%; Score 1729; DB 4; Best Local Similarity 97.9%; Pred. No. 6.8e-126; Matches 323; Conservative 3; Mismatches 4;
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                                                                                      GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
FILE REFERENCE: LEX-020
CURRENT APPLICATION WUMBER: US/10/310,719
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION WUMBER: 60/337,113
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR APLICATION WUMBER: 60/371,966
NUMBER OF SEQ ID NOS: 37
SOFFWARE: Patentin version 3.1
SEQ ID NO 8
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; OTHER INFORMATION: IgG1 constant region US-10-310-719-8
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Publication No. US20030166163A1
GENERAL INFORMATION:
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Best Local Similarity 97.9
Matches 323, Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: misc
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US-10-310-719-8
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Sequence 2, Application US/10408901

Sequence 2, Application US/10408901

Publication No. US20040023313A1

GENERAL INFORMATION:

APPLICANT: Boyle, William

APPLICANT: Bliot, Robin

APPLICANT: Bliot, Robin

APPLICANT: Martin, Francis

TITLE OF INVENTION: Inhibitors

TITLE OF INVENTION: Inhibitors

TITLE OF INVENTION: Inhibitors

FILE REFERENCE: MBHB 01-1145-A

CURRENT FILIAG DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2
                                                                                                                                                                                                    300
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        GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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Best Local Similarity 97.9
Matches 323; Conservative
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US-10-408-901-2
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US-10-408-901-2
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                                                                                                                                                                                                    Length 330;
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US-10-389-902A-6

i Sequence 6, Application US/10383902A

i Publication No. US20030224408A1

i GENERAL INFORMATION:

APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus

APPLICANT: Mulberg, Jurgen

APPLICANT: Mulberg, Jurgen

APPLICANT: Ladner, Robert C.

TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY

FILE REFERENCE: 10280-042001

CURRENT APPLICATION NUMBER: US 60/362,403

PRIOR PILLING DATE: 2003-03-07

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 330
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Pred. No. 6.8e-126;
3; Mismatches 4;
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PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 81
LENGTH: 330
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ORGANISM: Artificial Sequence
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Best Local Similarity 97.9%;
Matches 323; Conservative
                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Publication No US2004009712A1
GENERAL INFORMATION:
APPLICANT: Varnum, Brian
APPLICANT: Witte, Alison
APPLICANT: Witte, Alison
APPLICANT: Word, Lu Min
APPLICANT: Qian, Xueming
TITLE OF INVENTION: Therapeutic Human Anti-IL-IR Monoclonal Antibody
FILE REFERENCE: 01.1554
CURRENT APPLICANTON NUMBER: US/10/656,769
CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 79
SOOTWARE: PatentIn Version 3.0
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                                                       Length 330;
                                                                                                  Indels
                                                     98.0%; Score 1729; DB 4; 97.9%; Pred. No. 6.8e-126; iive 3; Mismatches 4;
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US-10-656-769-2
ORGANISM: Homo sapiens
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US-10-656-769-2
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APPLICANT: Liu, Jingi
APPLICANT: Na, Songding
APPLICANT: Na, Songding
APPLICANT: Na, Songding
APPLICANT: Sang, Derek Di
TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
FILLE REFERENCE: X-13992
CURRENT APPLICATION NUMBER: US/10/257,907
KURRENT APPLICATION NUMBER: 2002-10-16
NUMBER OF SEQ ID NOS: 5
SOPTWARE: Patentin version 3.0
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                                                                          APPLICANT: Presentl, Scott R.
APPLICANT: Xu, Wenfeng
APPLICANT: Xu, Wenfeng
APPLICANT: Wu, US20040029228Alak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Windsvogel, Wayne R.
APPLICANT: Kindsvogel, Wayne R.
APPLICANT: Klucher, Kevin M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
FILE REFERENCE: 02-10
CURRENT APPLICATION NUMBER: US/10/420,034A
CURRENT FILING DATE: 2003-04-18
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 330
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                   Sequence 15, Application US/10420034A Publication No. US20040029228A1 GENERAL INFORMATION:
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Publication No. US20040043022A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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US-10-420-034A-15
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LENGTH: 330
TYPE: PRT
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US-10-257-907-5
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Search completed: February 22, 2006, 22:03:08 Job time : 170.705 secs

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LENGTH: 330
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Sequence 3, Appli
Sequence 7, Appli
Sequence 164, App
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                                                         February 22, 2006, 21:58:19; Search time 17.0984 Seconds (without alignments) 287.324 Million cell updates/sec
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Sequence 5, Al
Sequence 6, Al
Sequence 4, Al
Sequence 71,
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Sequence 11,
Sequence 1, A
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1: /cgn2_6/ptodata/2/pubpāa/USG8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USG7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USG7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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US-11-022-289-11
US-11-075-35-1
US-11-165-141-15
US-11-102-621-3
US-11-102-621-3
US-11-124-620-1
US-11-124-620-1
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US-11-124-620-1
US-11-124-620-1
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US-11-123-681-1
US-11-123-691-6
US-11-123-961-6
US-11-123-961-7
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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68, Appli
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11, Appli
68, Appli
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Sequence 7
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Sequence 6
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Sequence 6
Sequence 5
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US-11-102-621-131
US-11-102-621-132
US-11-124-620-7
US-11-139-499-12
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US-11-139-499-12
US-11-102-621-70
US-11-102-621-67
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US-11-102-621-68
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US-11-102-621-120
US-11-102-621-131
US-11-102-621-131
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US-11-102-621-131
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US-11-102-621-131
US-11-102-621-131
US-11-102-621-131
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## ALIGNMENTS

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O'S-10-86-383-6

Sequence 6, Application US/10886383

Publication No. US20060005571A1

GENERAL INFORMATION:
APPLICANT: Hoffmann-La Roche Inc.
TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and use
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21695
FILE REFERENCE: 2004-07-08
FILE REPERENCE: 2004-07-08
FRIOR APPLICATION NUMBER: EP 03015526
FRIOR APPLICATION NUMBER: EP 03015526
FRIOR APPLICATION NUMBER: BO 33015526
FRIOR SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
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GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INTENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITE
; FILE REPERENCE: 185831/US/2 289
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; RIOR APPLICATION OF: 15
; SGC 1D NOS: 15
; SGC 1D NO 11
LENGTH: 330
; TYPE: PRI
; ORGANISM: Homo sapiens
US-11-022-289-11
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                                                            Query Match
98.0%; Score 1729; DB 6;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4;
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ORGANISM: Homo sapiens
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US-10-982-440-68
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US-11-022-289-11
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                                                                           Sequence 20, Application US/10493909

Publication No. US2006015569A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W.

ATTLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY

TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES

TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES

TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES

FILE REFERENCE: 41514-22004-01

CURRENT FILING DATE: 2004-04-26

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR PILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PATENTIN VEY: 2.1

SOFTWARE: PATENTIN VEY: 2.1
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241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRM 300
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Sequence 68, Application US/10982440

Publication NO 220060018909A1

GENERAL INFORMATION:

APPLICANT: Graham, Kohn

APPLICANT: Graham, Kajopoietin-2 Specific Binding Agents

TILE OF INVENTION: Angiopoietin-2 Specific Binding Agents

FILE REFERENCE: 04-881-A

CURRENT APPLICATION NUMBER: US/10/982,440

CURRENT FILING DATE: 2004-111-04

PRIOR APPLICATION NUMBER: 60/620,161

PRIOR APPLICATION NUMBER: 60/620,161

PRIOR FILING DATE: 2004-10-19

NUMBER OF SEQ ID NOS: 215

SOFTWARE: PatentIn version 3.3
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Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4;
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CORGANISM: Homo sapiens
US-10-493-909-20
                                                                        US-10-493-909-20
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LENGTH: 330
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APPLICANT: Hinton, Paul R.
APPLICANT: Tsurushita, Naoya
APPLICANT: Tsurushita, Naoya
APPLICANT: Tsurushita, Naoya
APPLICANT: Tsurushita, Naoya
APPLICANT: Tsurushita, Nazimilliano
TITLE OF INVENTION: ALTERATION OF FCR. BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 0582.0039.00PC03
CURRENT APPLICATION NUMBER: US/11/102,621
CURRENT APPLICATION NUMBER: US/11/102,621
FRIOR PRILING DATE: 2004-04-09
FRIOR FILING DATE: 2004-04-09
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Pred. No. 2.8e-132;
3; Mismatches 4;
                                                                                                                                                                                                                                                             Query Match 98.0%; Score 1729; DB 7; Best Local Similarity 97.9%; Pred. No. 2.8e-132; Matches 323; Conservative 3; Mismatches 4;
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PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/267,211
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 330
TYPE: PRI
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; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
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Best Local Similarity 97.9%;
Matches 323; Conservative
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US-11-165-141-15
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ORGANISM: Homo sapiens
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241 LITKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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                                                                                                                                                                                                           Sequence 1, Application US/11075351
| Publication Wo. US20050260716A1
| GENERAL INFORMATION:
| APPLICANT: Moore, Margaret D. APPLICANT: Fox, Brian A. |
| TILLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS |
| TILLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS |
| TILLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS |
| TILLE OF INVENTION: AND METHODS FOR PRODUCING THEM |
| FILE REFERENCE: 02-16 |
| CURRENT FILING DATE: 2005-03-08 |
| NUMBER OF SEQ ID NOS: 63 |
| SEQ ID NO 1 |
| ENGTH: 330
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PUDJICATION NO. US20050266485A1
GENERAL INFORMATION
APPLICANT: Presnell, Scott R.
APPLICANT: Novak, Julia E.
APPLICANT: Novak, Julia E.
APPLICANT: Novak, Julia E.
APPLICANT: WINGHING.
ITLE OF INVENTION: CTTOKINE RECEPTOR ZCYTOR19
FILE REPERENCE: 00-108
CURRENT APPLICATION NUMBER: US/11/165,141
CURRENT APPLICATION NUMBER: US/09/995,898
PRIOR FILING DATE: 2001-11-28
                                                             301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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US-11-075-351-1
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j Bedication No. US20060018903A1
GENERAL INFORMATION:
APPLICANT: HELLENDOORN, Koen
APPLICANT: BAKER, Matthew
TITLE OF INVENTION: TWE ALPHA-BINDING POLYPEPTIDE
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: MER-131
CURRENT APPLICATION NUMBER: US/11/005,726
CURRENT FILING DATE: 2004-12-07
PRIOR APPLICATION NUMBER: US/1266
PRIOR RAPLICATION NUMBER: PCT/FP02/12566
PRIOR FILING DATE: 2004-11-11
PRIOR FILING DATE: 2003-11-11
PRIOR FILING DATE: 2003-11-11
PRIOR FILING DATE: 2003-11-11
SPRIOR FILING DATE: 2003-11-12
SPRIOR FILING DATE: 2003-11-12
SPRIOR FILING DATE: 2003-11-13
SPRIOR FILING DATE: 2003-11-13
SPRIOR FILING DATE: 2003-11-13
SPRIOR FILING DATE: 2003-11-13
SPRIOR PRIOR DATE: 2003-11-13
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98.0%; Score 1729; DB 7;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4;
QOGNVFSCSVMHEALHNHYQORSLSLSPGK 330
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Publication No. US20060024298A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Dang, Wei
APPLICANT: Deng, Wei
APPLICANT: Refixi, Sher Bahadur
APPLICANT: Karki, Sher Bahadur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPB: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Hinton, Paul R.
APPLICANT: Hinton, Paul R.
APPLICANT: Hinton, Paul R.
APPLICANT: Teurushita, Naoya
APPLICANT: Teo. J. Yun
APPLICANT: Teo. J. Yun
APPLICANT: Vasquez, Maximilliano
TITLE OF INVENTION: ANTHODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.00PC03
CURRENT APPLICATION NUMBER: US/11/102,621
CURRENT FILING DATE: 2005-04-06
PRIOR FILING DATE: 2005-04-06
NUMBER OF SEQ ID NOS: 146
SOOFTWARE: Patentin version 3.2
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Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
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LENGTH: 330
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US-11-102-621-7
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Sequence 35, Application US/11024251
Publication No. US20050266425A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
APPLICANT: Paris, Mark
TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
FILE REPERENCE: 1843.023001.
CURRENT APPLICATION NUMBER: US/11/024,251
CURRENT PILING DATE: 2004-12-29
PRIOR APPLICATION NUMBER: 60/533,241
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
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                                                                                                                                          ; NAME/KEY: misc feature
; OTHER INFORMATION: human 1g gamma heavy chain C region
US-11-233-683-1
                                                                                                                                                                                                                                                        Score 1729; DB 7;
Pred. No. 2.8e-132;
3; Mismatches 4;
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Best Local Similarity 97.9%;
Matches 323; Conservative
                        LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
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SEQ ID NO 1
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Publication No. US20060025573A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
FILE REFERENCE: LEX-017
CURRENT APPLICATION NUMBER: US/11/233,683
CURRENT FILING DATE: 2005-09-23
PRIOR APPLICATION NUMBER: US 60/280,625
PRIOR PLING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
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Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4;
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               TITLE OF INVERTION. OPTIMIZED FC VARIANTS
FILE REFERENCE: A-7136-6.
FILE REFERENCE: A-7136-6.6.
CURRENT APPLICATION NUMBER: US/11/124,620
CURRENT FILING DATE: 2005-65-05
PRIOR FILING DATE: 2005-07-15
PRIOR FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US 60/589,906
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: US 60/626,991
PRIOR FILING DATE: 2004-11-09
PRIOR FILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-11-10
PRIOR FILING DATE: 2004-11-12
PRIOR FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US 60/627,774
PRIOR PRILING DATE: 2004-11-12
PRIOR PRILING DATE: 2004-03-26
PRIOR PRILING DATE: 2004-03-26
PRIOR PRILING DATE: 2003-03-6
PRIOR PRILING DATE: 2003-03-6
PRIOR PRILING DATE: 2003-03-6
PRIOR PRILING DATE: 2003-03-6
PRIOR FILING DATE: 2003-03-6
PRIOR SEQ ID NOS: 11
PRIOR FILING DATE: 2003-03-03
PRIOR PRILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 10/672,280
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 10/672,280
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US-11-233-683-1
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LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFPLYSKLTVDKSRW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                   Sequence 6, Application US/11173969
; Sequence 6, Application US/11173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REPERENCE: 1/121
; CURRENT APPLICATION UNMBER: US/11/173,969
; CURRENT FILING DATE: 2005-07-01
; PRIOR PAPLICATION NUMBER: US/01/150,475
; PRIOR PAPLICATION NUMBER: US 60/307,451
; PRIOR APPLICATION NUMBER: US 60/307,451
; RING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1729; DB 7; Length 4
Pred. No. 4e-132;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 161, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: HELLENDOORN, Koen
; APPLICANT: GARR, Francis J.
; TITLE OF INVENTION: TOF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-13
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/45,146
; PRIOR PLILING DATE: 2004-05-10
; PRIOR PLILING DATE: 2004-05-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative
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                                                                                                                                   245
                                                                                                                                                                         115 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSS 174
                        | PUDICACION NO. US20050244413A1
| GENERAL INFORMATION:
| APPLICANT: Adolf, Guenther
| APPLICANT: Baum, Anke
| APPLICANT: Baum, Anke
| APPLICANT: Baum, Anke
| APPLICANT: Baum, Anke
| APPLICANT: Heider, Karl-Heinz
| TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
| TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
| TITLE OF INVENTION: Chemotherapeutic Agents
| TITLE OF INVENTION: Chemotherapeutic Agents
| FILE REFERENCE: 1/1383
| CURRENT APPLICATION NUMBER: US/10/645,215
| PRIOR APPLICATION NUMBER: US 003-08-21
| PRIOR APPLICATION NUMBER: US 60/405,956
| PRIOR FILING DATE: August 21, 2002
| PRIOR FILING DATE: August 26, 2002
| SOFTWARE: Patentin Ver. 2.1
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                                                                                          STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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                                                                                                            186 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
      PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
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, OTHER 10.FG Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 444;
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98.0%; Score 1729; DB 7;
Best Local Similarity 97.9%; Pred. No. 4e-132;
Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                        306 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 335
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/11172320; Publication No. US20050244413A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                             ; OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain US-11-005-726-161
                                                                                                                        Query Match 98.0%; Score 1729; DB 7; Length 450; Best Local Similarity 97.9%; Pred. No. 4.1e-132; Matches 323; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2002-11-11
PRIOR APPLICATION VUMBER: EP 01126658.8
FRICH FILING DATE: 2001-11-12
NUMBER OF SEQ ID NOS: 165
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 161
LENGTH: 450
TYPE: PRT
FRATURE: Artificial Sequence
FRATURE:
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Search completed: February 22, 2006, 22:03:44 Job time : 19.0984 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

- protein search, using sw model OM protein February 22, 2006, 21:31:15; Search time 23.6408 Seconds (without alignments) 944.229 Million cell updates/sec Run on:

US-10-000-439-3 1260 Title: Perfect score:

1 EPKSCDKTHTCPPCPAPELL.......MHEALHNHYQQRSLSLSPGK 232 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Regult No.	Score	Query Match	Length	DB	ID	Description
7	1225	97.2	330	-	GHHU	Ig gamma-1 chain C
7	1219	96.7	374	7	869339	heavy ch
٣	1217	96.6	255	4	S31866	gamma-
4	1172	93.0	234	~	PT0207	ដ
ß	1138	90.3	377	~	A23511	gamma-3 chain
9	1136	90.2	377	~	A60764	
7	1123	89.1	289	٦	G3HUWI	gamma-3 heavy
æ	1107	87.9	326	ч	G2HU	gamma-2
σ	1097	87.1	327	ч	G4HU	gamma-4 chain
10	883	70.1	323	ч	GHRB	gamma ch
11	868.5	68.9	328	~	147160	
12	868.5	68.9	328	~	147159	
13	865	68.7	277	~	147162	gamma 4 c
14	858	68.1	329	-	G2GP	gamma-2
12	847.5	67.3	328	~	147158	gamma 1
16	840.5	66.7	328	~	147161	gamma
17	820	65.1	470	~	S22080	
18	813	64.5	333	~	PS0018	gamma-
19	812.5	64.5	329	-	G3MSC	
20	811.5	64.4	308	~	C30554	heavy ch
21	811.5	64.4	472	N	S31459	
22	801.5	63.6	398	-	G3MSM	gamma-3 chai
23	794.5	63.1	444	~	PC4436	c
24	789.5	62.7	324	٦	GIMS	1 chai
25	784.5	62.3	326	~	PS0017	gamma-1 chai
56	784.5	62.3	393	Н	GIMSM	
	776.5	61.6	329	~	S00847	gamma-2c
28	116	61.6	330	-	G2MSA	
53	176	61.6	469	~	S37483	gamma-2a

ď	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma heavy cha	Ig heavy chain WHI	Ig heavy chain V-I	Ig gamma-1 chain C	Ig Y heavy chain (	Ig heavy chain pre	Ig mu chain C regi	Ig mu chain C regi
G2MSAB	G2MSAM	S40295	G2MS11	PS0019	GZMSBM	806611	501321	146732	S69340	A36040	S14236	B46529	S04845	525644	MHMS
Н	-	7	-	N	н	~	~	~	7	~	~	N	~	7	-
335	399	446	474	322	405	327	475	180	249	218	152	572	549	343	455
61.3	61.2	60.4	9.65	59.3	59.2	58.3	58.1	53.1	43.6	43.4	43.0	29.1	28.3	28.0	28.0
772	771	191	751.5	747.5	746.5	735	731.5	699	549	547	542	366.5	357	353	353
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Tig gamma-1 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text\_change 09-Jul-2004 C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison J.W.; Berson, B.J.; Hood L.E. Nucleic Acids Res. 10, 4071-14079, 1982 A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.

A; Accession: A93433

A;Molecule type: DNA A;Residues: 1.330 «ELL» A;Cross-references: UNIPROT:P01857; UNIPARC:UP10000034C0E; EMBL:217370 A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, A;Note: Lys-330 is removed after translation

RiHarris, L.J.

Submitted to the EMBL Data Library, October 1992

A; Reference number: S33904

A; Accession: S3861

A; Molecule type: DNA

A; Residues: 2-330 c4ARA

A; Residues: 2-330 c4ARA

A; Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

B; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of a A; Reference number: S33887; MUID:83001943; PMID:6811139

A; Molecule type: DNA
A; Residues: 88-113;235-330 cTAK>
A; Residues: 88-113;335-330 cTAK>
A; Residues: 88-113;335-330 cTAK>
A; Residues: 88-113;335-330 cTAK>
A; Residues: 88-113;335-330 cTAK>
A; Cross-references: UNIPARC:UP1000017378B; UNIPARC:UP1000017378C; EMBL:Z17370
R; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B; ochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequer A; Reference number: A90563; MUID:71064024; PMID:5489771
A; Contents: myoloma protein Bu A; Contents: myoloma protein Bu A; Residues: 1-56, R.; 98-135 cUNA
A; Resi

A; Accession: A90564

A;Molecule type: protein A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240, A;Cross-references: UNIPARC:UPI000017378E A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met R;Ponstingl, H: Hilschmann, N.

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Ig gamma-1 chain C region - synthetic
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A. Introns: 99/1; 114/1; 224/1
A. Introns: 1 memunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; 9Jycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IM2>
F; 243-310/Domain: immunoglobulin homology <IM3>
F; 247-83, 144-204, 250-308/Disulfide bonds: #status experimental
F; 103/Disulfide bonds: interchain (to light chain) #status experimental
F; 103/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 109/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A, McCeesulanni, Asilvia.

A, Residues: 1-96, "K', 98-197, "D', 199-238, "E', 240, "M', 242-266, "D', 268-271, "D', 273-330 < SCH 
A, Residues: 1-96, "K', 98-197, "D', 199-238, "E', 240, "M', 242-266, "D', 268-271, "D', 273-330 < SCH 
A, Acrose-references: UNIPARC: UP10000173790

A, Monte: this sequence has the Glm(3) and Glm(non-1) markers

B, Gall, W.E.; Edelman, G.M.

A, 186-1196, 1318-3196, 1370, 1318-3144

A, Reference number: A90565; MUID: 71064027; PMID: 4923144

A, Reference number: A90565; MUID: 71064027; PMID: 4923144

B, Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A, Fitle: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob enbromide cleavage products, and the disulfide bridges.

A, Reference number: A91667; MUID: 77070267; PMID: 1002129

A, Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                  KÖ
                                                                                                                                                                                                                                     , 27
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)
igen Primaerstruktur.
                                                                                                                                                                                                       A, Molecule type: protein

A, Residues: 1-34, 'O', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',

A, Cross-references: UNIPARC: UP1000017378F

A, Note: this sequence has the GIM(1) and GIM(1) markers

A, Note: this sequence has the GIM(1) and GIM(1) markers

B; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 PA; Reference number: A91723; WUID: 83289131; PMID: 6884994

A; Contents: myeloma protein KOL; disulfide bonds
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                                                                                                           A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
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A;Cross-references: GDB:120085; OMIM:147100
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Ig heavy chain V region precursor - human C, Species: Homo sapiens (man)

RESULT 2

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C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000 C; Accession: $69339; $72664  
R; Akhanlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M. Eur. J. Biochem: 229; 54-60, 1995  
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A; Reference number: $69339; MUID:95262687; PMID:7744049  
A; Accession: $56339  
A; Accession: $56339  
A; Molecule type: mRNA  
A; Residues: 1-374 < KHA>  
A; Cross-references: UNIPARC:UPIO000176F24; EMBL:X81695  
B; Khamlichi, A.A.  
Bubmitted to the EMBL Data Library, September 1994  
A; Accession: $72664  
A; Accession: $72664  
A; Accession: $72664  
A; Redecule type: mRNA  
A; Residues: 1-140, CC; HIZ-374 < KHZ>  
A; Molecule type: mRNA  
A; Residues: 1-140, CC; HIZ-374 < KHZ>  
A; Residues: 1-140, CC; HIZ-
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C;Species synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
R;Filpula, D.
A;Description: Screeing method for protein-protein interactions of cloned gene products
A;Reference number: S31866
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A;Molecule type: mRNA
A;Residues: 1-255 <FILD-
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068;
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
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A;Cross-references: UNIPARC:UP1000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1217; DB 4; Length 2:
Pred. No. 4.9e-85;
3; Mismatches 5; Indels
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96.7%; Score 1219; DB 2;
Best Local Similarity 96.1%; Pred. No. 5.5e-85;
Matches 223; Conservative 5; Mismatches 4;
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Ig gamma-3 heavy chain disease proteins - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A90442; A92219; A90198; A93915; A02149
C;Accession: A90442; A92219; A90198; A93915; Prenklin, E.C.
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
A;Chille: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A;Contents: heavy chain disease protein Wis
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Accession: A90442
A;Residues: 1-289 <FRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma-3 chain C region, form LAT - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an 1 A;Reference number: A60764; MUID:90007613; PMID:2571587
                                                                                                                                                                                  206 KWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                        146 BPKSCDTPPPCPRCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQP
                                                                                                                                                                                                                                                                                               266 ISKTKGOPREPOVYTLPPSKEEMTKNOVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 ISKTKGQPREPQVYTLPPSREEMTKNOVSLTCLVKGPYPSDIAVEWESSGQPENNYNTTP
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                                                                                                                                                         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                          181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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13; Indels
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
C;Superfamily: immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 1136; DB 2;
; Pred. No. 1.1e-78;
11; Mismatches 13;
11; Mismatches
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Best Local Similarity 89.7%;
Matches 208; Conservative 1:
208; Conservative
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Best Local Similarity
Matches
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: CA;Recession: A23511; MUD:86148507; PMID:3081877
A;Recession: A23511
A;Molecule type: DNA
A;Recission: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Recission: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Genetics:
A;Genetics:
A;Genetics: A;Galaga: A3-14432.33-14632.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                              Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: Pr0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: Pr0207
A;Molecule type: mRNA
A;Residues: 1-234 <ERNA
A;Residues: 1-234 <ERNA
A;Residues: 1-234 <ERNA
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <INMA>F;48-117/Domain: immunoglobulin homology <INMA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 EPKSCDTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 69
                           1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                              181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 255
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Best Local Similarity 95.6%; Pred. No. 1.1e-81;
Matches 215; Conservative 4; Mismatches 6;
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Best Local Similarity
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A Molecule type: DNA
A; Residues: 1-326 < ELL.)
A; Residues: 1-326 < ELL.)
A; Residues: 1-326 < ELL.)
A; Croses.references: UNIPROT: P01859; UNIPARC: UPI000003BFCC; GB: V00554; GB: J00230; NID: g3. A; Croses.references: Uniproperty, R.H.
B; Wang, A.C.; Tung, B.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and in A; Reference number: A92809; WIUD: 81007873; PMID: 6774012
A; Crosesion: A92809
A; Accession: A92809
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Keywords: immunoglobulin homology <IM3-
F; 20.6 **Domain: immunoglobulin homology <IM3-
F; 20.9 **Of Domain: immunoglobulin homology <IM3-
F; 219-306/Domain: immunoglobulin homology <IM3-
F; 219-306/Domain: immunoglobulin homology <IM3-
F; 219-306/Lide bonds: interchain (to light chain) #status experimental
F; 27-83; 140-200, 246-304/pisulfide bonds: #status experimental
F; 27-83; 105, 106, 109/Disulfide bonds: #status experimental
F; 27-85; 205, 206, 209/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 27-85; 205, 103, 206, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
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A; Residues: 1-24, E'. 26-57, EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A; Residues: 1-24, E'. 26-57, EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A; Cross-references: UNIPARC: UPI0000173792; UNIPARC: UPI0000173793
A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
R; Hofmann, T.; Parr, D.M.
A; Hofmann, T.; Parr, D.M.
A; Hote on the amino acid sequence of residues 381-391 of human immunoglobulin and A; Reference number: A93132; MUID: 80114419; PMID: 118920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 < WAN>
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 < WAN>
A; Rote: Trp-156 is at vorte complement-binding site
A; Note: Trp-156 is at vorte complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of
A; Reference number: A90752; MUID: 80001357; PMID: 113060
A; Rotession: A90752
A; AACCESSION: A90752
           C, Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004 C; Accession: A93906; A92809; A90752; A93132; A02148 R; Ellison, J.; Hood, L. R; Ellison, J.; Hood, L. Aproc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982 A; Title: Linkage and sequence homology of two human immunoglobulin gamma heavy A; Reference number: A93906; MUID:82197621; PMID:6804948
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immu A;Reference number: A90253; WUID: 22033501; PMID: 440472
A;Contents: annotation; myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L.
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID: 69064124; PMID: 5782707
A;Contents: annotation; Sa, disulfide bonds
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A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
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A;Residues: 238-275 <HOF>
A;Cross-references: UNIPARC:UF10000173794
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                                                                                                                                                                                                                                                                                                                                                             A; Accession: A93906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Contents: Zie
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A;Rolecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Acces-references: UNIPARC:UP10000173795, UNIPARC:UP1000017379C;
A;Note: a carboxyl-terminal Lys removed posttranslationally
A;Note: this sequence may represent a nallelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Genetics: A;Genetics:
A;Cross-references: UNIPARC:UPI0000173797
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cd A;Note: the sequence of residues 42-76 was taken from the reference that follows R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication A;Reference number: A92219; MUID:77118561; PMID:402363
A;Cochests: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W A;Accession: A92219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 idue segment (12-28)
A,Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R,Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, B.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A,Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A,Reference number: A90198; WUID:77021516; PMID:823945
A,Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 59-125, EB: 1.128-226, 228-289 < WOL>
A; Residues: 59-125, EB: 1.128-226, 228-289 < WOL>
A; Cross - references: UNIPARC: UDFO000173799
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of the R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion A; Reference number: A93915; MUID: 82247835; PMID: 6808505
A; Contents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Realdues: 12-97 cMICA
A;Cosalceferences: UNIPARC:UP10000173798
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Gener GDB: IGHG3
A; Gener GDB: IGHG3
A; Gener GDB: I19339; OMIM: 147120
A; Map position: 14432.33-14432.33
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
C; Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F; A; Obomain: immunoglobulin homology clMh.
F; 1/ Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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88.3%; Pred. No. 7.5e-78;
iive 14; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 88.3
Matches 204; Conservative
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DB 1; Length 326;

87.9%; Score 1107;

Query Match

Ig gamma-2 chain C region - h C;Species: Homo sapiens (man)

G2HU

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Ig gamma chain C region - rabbit (Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cipate: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
Cipate: 24-Apr-1984 #sequence_revision Nov-1984 #text_change 09-Jul-2004
Cipatession: A91749; A90290; A39928; A90345; A34416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
A;Fitle: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplow A;Reference number: A91749; MUID:84030930; PMID:6313520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-323 <BBR>
A; Cross-references: UNIPROT: P01870; UNIPARC: UPI000012B37D
A; Cross-references: UniPROT: P01870; UNIPARC: UPI00012B37D
A; Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
B; Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A; Title: Sequence studies on the constant region of the Fd sections of rabbit immunogloi
A; Reference number: A90290; MUID: 76135469; PMID: 1243651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A;Residues: 1-47, E'. 49-71, PV', 72-128 <PRA>
A;Residues: 1-47, E'. 49-71, PV', 72-128 <PRA>
A;Cross-references: UnlyARC:UP1000173AB
B;Across-references: UnlyARC:UP1000173AB
Broc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy Chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A;Reference number: A93928; MUID:83299917; PMID:6193512
A;Accession: A93928
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A; Residues: 88-103, 'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A; Residues: 88-103, 'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A; Cross-references: UNIPARC:UP10001065EB; GB:M16426; UNID:g165111; PIDN:AAA31289.1; PID
A; Note: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic mark-
R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
A; Fruchter, R.G.; Jackson, S.A.; MUD: Tollools; PMID:5461106
A; Accession: A90245; MUD:70110015; PMID:5461106
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A; Cross-references: UNIPARC:UP100001737AB.
A; Note: this has the e15 allotypic marker, 185-Ala a; Note: this has the e15 allotypic marker, 185-Ala a; Note: this has the e15 allotypic marker, 185-Ala a; Note of two identical light (kai bain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l'c; Superfamily: immunoglobulin c region; immunoglobulin homology c; Keywords: duplication; allotyprotein; immunoglobulin
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A,Residues: 133-143, E',145-161 <FRU>
A,Residues: 133-143, E',145-161 <FRU>
A,Crose-references: UNIPARC:UPI00001737AC
R;Hill, R,L.; Lebovitz, H.E.; Pellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, A,Reference number: A94416
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                                         226 PQVYTLPPSQBEWTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 285
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F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;133/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Indels
                                                                                                                                                                                         LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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; Pred. No. 1.3e-59;
34; Mismatches 38;
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Best Local Similarity
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           131
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B.Ellison, J.; Buabaum, J.; Hood, L.

B.R. 1, 11-18, 1981

A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A;Reference number: A9033; MulD: 83157104; PMID: 6299662

A;Rolecule rype: DNA

A;Residues: 1-127 *ELL

A;Residues: 1-127 *ELL

A;Residues: 1-127 *ELL

A;Residues: 1-127 *ELL

A;Reference number: A90449; MULD: 901861; UNIPARC: UPIO00047190

A;Residues: 1-107 *BLCATY, S.H.; De Vries G. M.; Milstein, C.

B;Pink, J.R.L.; Buttery, S.H.; De Vries G. M.; Milstein, C.

A;Reference number: A90249; MULD: 70207560; PMID: 4192699

A;Ablceule Pype: prorein

A;Reference number: A90249; MULD: 70207560; PMID: 4192699

A;Ablceule Pype: prorein

A;Residues: 1-30, 11-32

A;Ablceule Pype: prorein

A;Residues: 1-30, 11-33

A;Ablceule Pype: prorein

A;Residues: 1-30, 11-32

A;
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                                                                                                                                                              NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                   121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                    4 ;
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87.1%; Score 1097; DB 1; Length 327;
Best Local Similarity 90.5%; Pred. No. 8.1e-76;
Matches 201; Conservative 11; Mismatches 10; Indels (
                                             Indels
No. 1.4e-76;
ematches 11;
       Best Local Similarity 88.4%; Pred. No. 1.4e-
Matches 205; Conservative 12; Mismatches
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A;Cross-references: UNIPARC:UP10000115524; EMBL:U03779; NID:g433123; PIDN:AAA52217.1; P:C;Genetics:
C;Genetics:
A;Gene: 19G2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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Matches 158; Conservative
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Best Local S
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;Kacsekovics, I.; Sun, J.; Butler, J.E.
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Tetue: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 147160
A;Etatue: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Accessidues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:g433125; PIDN:AAA52218.1; EC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 147159
R;Kacskovics, I:, Sun, J:, Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147159, MUID:95015845; PMID:7930579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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                               104
                                                  164
                                                                                                                       196 KCKVHNKALPAPIEKTISKARGOPLEPKVYTMGPPREELSSRSVSLTCMINGPYPSDISV 255
                                                                                                                                                                                EWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQR 224
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                               TCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEY
                                                                                                       KCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
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Matches 157;
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A,Cross-references: UNIPARC:UP10000115527; EMBL:U03782; NID:9433129; PIDN:AAA52220.1;
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Igilia

Igilia

Igigamma 4 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Species: 11: Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: I47162

R;KacsKovics, I; Sun, J; Butler, J.E.

R;KacsKovics, I; Sun, J; Butler, J.E.

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences

A;Reference number: I47158; MUD:95015845; PMID:7930579

A;Accession: I47158; MUD:95015845; PMID:7930579

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-277 < KAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 GOTREPOVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWORNGOPEPEGNYRTTPPQQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
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C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                   106 CPICPACE-SPGPSVPIPPPKPKDTLMISRIPQVICVVVDVSQENPEVQFSWYVDGVEVH
                                                                                                                                                                                                                         71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE
                                                                                                                                                                                                                                                                                                                                       POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO--PENNYKTTPPVLDSVGS
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                                                                                                           CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
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                                                       Gaps
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Length 328
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A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
F;82-151/Domain: immunoglobulin homology <IMM>
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                                                    Indels
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Query Match 68.9%; Score 868.5; DB 2; Best Local Similarity 70.1%; Pred. No. 1.6e-58; Matches 157; Conservative 32; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.7%; Score 865; DB 2;
69.0%; Pred. No. 2.5e-58;
ive 32; Mismatches 35;
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RESULT 15
147158
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15 gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Title: Proteininary; translated from GB/EMBL/DDBJ
A;Rosiouse: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Mol
217 ISKTKGAPRMPDVYTLPPSRDELSKSKVSVTCLIINFPPADIHVEWASNRVPVSEKEYKN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 HTAETRPKEEQFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGO--PENNYKTTPPVLDSVG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
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                                                                                                                                179 TPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYQQRSLSLSPG 231
                                                                                                                                                                                   277 TPPIEDADGSYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
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69.3%; Pred. No. 6.4e-57;
tive 30; Mismatches 36; Indels 3
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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Matches 156; Conservative
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A. Croas-references. WINTROM: P01862, UNIPARC: UP1000017379E
B. Bitcheen B. Kr. i Musain, 0.2.; Cebra, J.J.
B. A. Croas-references. UNIPARC: UP1000017379F
B. M. Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am. A. Molecule type: protein
A. McGession. A00352
A. Molecule type: protein
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F;241-310/Domain: immunoglobulin homology <IM3>
F;24-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;148/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;148/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Accession: A94553; A90352; A90359; A90384; A90385; A02151
                                              R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 31-JAN-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETR G.

REGISTRATION NUMBER: 32,837

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: 32,837

TELEPHONE: (415) 705-8410

TELEPHONE: (415) 705-8410

INFORMATION FOR SEQ 1D NO: 50:
                                                                                                                                                                                                                                                                                        US-08-595-043A-50

Sequence 50, Application US/08595043A

Patent No. 5935824

GENERAL INCOMMITION:

APPLICANT: SCARLATO, GREGORY D.

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL

STREET: 220 MONTCOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALLFORNIA

COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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Pred. No. 3.5e-116;
3; Mismatches 4;
 JS-10-104-047-3730
          US-09-740-002-27
US-08-378-939-10
US-08-487-550-14
US-09-526-098-4
US-09-526-098-12
US-09-383-916-12
US-09-758-173-14
US-09-758-173-14
US-09-758-173-12
US-09-758-173-12
US-09-758-173-12
US-09-758-173-12
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US-09-758-173-12
US-09-758-173-12
US-09-576-424-12
US-09-576-424-12
US-09-576-424-12
US-09-576-424-12
US-09-758-173-8
US-09-758-173-8
                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 97.0
Matches 225; Conservative
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556.619 Million cell updates/sec
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                                                                                  February 22, 2006, 21:37:34; Search time 34.4594 Seconds
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1 BPKSCDKTHTCPPCPAPELL........MHRALHNHYQQRSLSLSPGK 232
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            GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-178-869-2
US-09-761-413-2
US-09-949-713-11
US-08-26-311-7
US-08-457-918-7
US-10-157-408-7
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US-09-968-362A-26
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PCT-US95-03866-14
PCT-US96-10043-11
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US-08-030-175-42
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US-09-176-228-3
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Maximum Match 100%
Listing first 45 summaries
                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                             1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKF
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Length 232;
                                                      4; Indels
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  Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 3.5e-116; Matches 225; Conservative 3; Mismatches 4;
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97.0%; Pred. No. 5.9e-116;
iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09178869B; Patent No. 6197294; GENERAL INFORMATION:
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Patent No. 6797493

GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill
APPLICA
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     61 NWYUDGVEVHNYKTKPREEQYNSTYRVVSVLTVLHQMMMGKEYKCKVSNKALPAPIEKT 120
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| Sequence 26, Application US/09932812A
| Sequence 26, Application US/09932812A
| Patent No. 6900292
| GABERAL INFORMATION:
| APPLICANT: Sun, Lee-Hwei K
| APPLICANT: Sun, Cecily R
| TILLE OF INVENTION: For fusion proteins of human erythropoietin with
| TILLE OF INVENTION: activities
| TILLE OF INVENTION: activities
| FILLE REPREBUECE 0.025U0.001
| CURRENT APPLICATION NUMBER: US/09/932,812A
| CURRENT FILING DATE: 2001-08-17
| SOPTHANDE OF SEQ ID NOS: 28
| NUMBER OF SEQ ID NOS: 28
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US-09-968-362A-26
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SEQ ID NO 26
LENGTH: 232
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181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATIN GREEN PC-DOS/MS-DOS
APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
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Patent No. 5565335
GENERAL INPORMATION:
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
TITLE OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STRATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-949-713-11
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        APPLICANT: Baeteg. E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/761,413
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/09/178,869
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 331
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| Patent No. 6306395
| GENERAL INFORMATION:
| APPLICANT: NAKAWIRA, No. 630639510
| APPLICANT: NAKAWIRA, Shigekazu
| TITLE OF INVENTION: NOVEL FAB ANTIGEN DERIVATIVE
| FILE REFERENCE: 1110-207P
| CURRENT FILING DATE: 1998-11-02
| EARLIER PELLICATION NUMBER: US/09/180,100
| EARLIER FILING DATE: 1997-05-01
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 11
| LENGTH: 360
| TYPE: PRT
| CRGANISM: Homo sapiens
| US-09-180-100-11
                                                                                                                                                                                                                                                                                                                                     Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 5.9e-116; Matches 225; Conservative 3; Mismatches 4;
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Hammang, Joseph P.
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US-09-180-100-11
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                           309 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYYQKSLSLSPGK 360
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                                                                                                                                                                                 Sequence 11, Application US/09949713
; Batent No. 6953847
; GENERAL INFORMATION:
APPLICANT: NAKAWURA, No. 6953847io
; APPLICANT: NAKAWURA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 11

LEMETH: 360

LEMETH: 360
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121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTP 180
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 6.9e-116; Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Capon, Daniel J.
Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
 Sequence 7, Application US/10157408 Patent No. 6710169 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: USA
1-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-157-408-7
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97.0%; Pred. No. 6.9e-116;
tive 3; Mismatches 4;
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREIN PC-DOS/MS-DOS
ASPELICATION DATA:
APPLICATION NUMBER: US/08/457,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Geneattech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                        Sequence 7, Application US/08457918 Patent No. 6117655
   02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.0%
Matches 225; Conservative
              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Length 371;

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205 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264
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                                                                                                                                                                                                                                                                                        205 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                     Length 376;
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                                                                                                                    Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2.2, Application US/09949713
; Sequence 2.2, Application US/09949713
; Parent No. 6953847
; GRNERAL INFORMATION:
; APPLICANT: NAGAMURA, No. 6953847io
; APPLICANT: NAGAMURA, No. 6953847io
; TILLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILLE REPERBNCS: 1110-207P
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR FILING DATE: 1998-11-02
; RIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PATENTIN VET: 2.0
                                                                     Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 7.1e-116; Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.2%; Score 1225; DB 2; Best Local Similarity 97.0%; Pred. No. 7.1e-116; Matches 225; Conservative 3; Mismatches 4;
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US-10-679-999-9
'Sequence 9, Application US/10679999
'Patent No. 6936439
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-09-949-713-22
    ORGANISM: Homo sapiens
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              us-09-180-100-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 NWYVDGVEVHNAKTKPREEGYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAKAMURA, NOVEL FAB ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P;
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: 376
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                                                                                                          PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/33311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-MG-1992
APPLICATION NUMBER: 07/936190
FILING DATE: 28-EB-1992
APPLICATION NUMBER: 07/550785
FILING DATE: 28-EB-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 28-EB-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 28-EB-1987
ATTORNEY/AGENT INFORMATION:
NAME: KUDINEC, JEffery S.
REGISTRATION NUMBER: 36,575
RETERENCE/DOCKET NUMBER: 36,575
TELEBCOMMUNICATION:
TELEBCOMMUNICATION:
TELEBCOMMUNICATION:
TELEBCOMMUNICATION:
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,408
FILING DATE: 28-May-2002
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-157-408-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 371 amino acids
TYPE: amino acid
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-180-100-22
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MOLECULE TYPE: protein
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; LOCATION: 1..396
US-08-784-512-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                            COUNTY: USA

ZIE: 9120-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/679,999
FILING DATE: 06-Oct-2003
CLASSIFICATION OF COMPANIENT 
                        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "Met (ATG) starts at SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                 NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
STREET: 1840 DeHavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Knight, Matthew W.
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-416
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 379 amino acida
TYPE: amino acid
STRANDEDNESS: unknown
APPLICANT: Mann, Michael B.
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                                                                                                                                                                                                                                                                                                           CITY: Thousand Oaks STATE: CA
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OTHER INFORMATION:
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Best Local Similarity 97.0
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-679-999-9
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Sequence 3, Application US/08784512 Patent No. 5872209 GENERAL INFORMATION: APPLICANT: BARTNIK, Eckart APPLICANT: BIDENWIELLER, Bernd APPLICANT: BUSTINER, Prank

US-08-784-512-3

RESULT 14

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TITLE OF INVESTION: GUIREDOC, Bruce
INTEL OF INVESTION: A satisficial recombinant substrate (LAGG 1)
ITILE OF INVESTION: Adaptement in call culture systems
CONSESSIONERS: Adaptement in call culture systems
CONSTRUCT: Natural Day Consenting Consessioners: Conserved C
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APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant of study the proteolytic activity of TITLE OF INVENTION: "Aggrecanase" in cell culture systems
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Sulte 500, 3000 K Street, N.W.
COUNTRY: USA
ZITY: Washington, D.C.
COUNTRY: USA
ZITY: Washington, D.C.
COUNTRY: USA
ZITY: PRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: US/09/176,228
FILLING DATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/784,512
FILLING DATE: 17-ANN-1996
ATTORNEY/AGRATI INFORMATION:
PRESISTRANCE/OCKET NUMBER: 33,683
REGISTRATION NUMBER: 33,683
RESERRANCE/OCKET NUMBER: 33,683
RESERRANCE/OCKET NUMBER: 33,683
RESERRANCE/OCKET NUMBER: 33,683
TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: February 22, 2006, 21:39:49
Job time : 35.4594 secs
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| INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 396 amino acids TYPE: amino acids STRANDEDNESS: single "non'OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: Protein
; LOCATION: 1..396
US-09-176-228-3
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14, Appl 14, Appl 14, Appl 14, Appl 14, Appl 16, Appl 15, Appl 15, Appl 16, Appl 11, Appl 11, Appl 11, Appl 11, Appl 6, Appl 6, Appl 11, Appl 6, Appl 11, Appl 6, Appl 11, Appl 11

Sequence

Sequence Sequence Sequence

Sequence

Sequence

Sequence

Sequence 20, Sequence 68, Sequence 8,

Sequence

Sequence

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121 ISKAKVQPREPQVYTLPPSKDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09847208
| Publication No. US20030082190A1
| GENERAL INPORMATION:
| APPLICANT: Saxon, Andrew
| APPLICANT: Zhang, Ke
| APPLICANT: Zhu, Daocheng
| TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
| TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
| FILE REFERENCE: UC67.002A
| CURRENT APPLICATION NUMBER: US/09/847,208
| CURRENT APPLICATION NUMBER: 2010-05-01
| NUMBER OF SEQ ID NOS: 177
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-10-000-439-3
Sequence 3, Application US/10000439
Publication No. US20030064063A1
GENERAL INFORMATION:
APPLICANT: BAXON, Andrew
TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1260; DB 3;
100.0%; Pred. No. 1.1e-92;
ive 0; Mismatches 0;
US-09-822-851B-14
US-10-119-637A-14
US-11-1018-102-1
US-11-129-083-14
US-11-129-495-14
US-11-129-090-14
US-11-129-090-14
US-10-129-090-14
US-10-38-380-37
US-09-995-898A-37
US-09-995-898A-37
US-09-892-949-38
US-10-047-542-20
US-10-047-542-20
US-10-047-542-20
US-10-125-805-68
US-10-310-719-8
US-10-3120-231A-81
US-10-320-231A-81
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    , ORGANISM: Homo sapiens
US-09-847-208-3
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    232;
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    Query Match
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1 EPKSCDKTHTCPPCPAPELL.......MHEALHNHYQQRSLSLSPGK 232
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(cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-91-61-7

US-10-61-61-7

US-10-61-61-7

US-10-61-94-26

US-10-604-21-97

US-10-67-56-684

US-11-016-518A-26

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US-11-018-102-11
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Maximum Match 100%
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Length 232; Indels 120

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219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Publication No. US20030082190A1

GENERAL INFORMATION

APPLICANT: Shang, Ke

APPLICANT: Zhang, Ke

APPLICANT: Zhang, Ke

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: USE-MEDIATED ALLERGIC DISEASES

FILE REFERENCE: UC67.002A

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177

SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                         Sequence 2, Application US/10000439;
Publication No. US20030064063A1
GENERAL INPORMATION:
APPLICANT: Saxon, Andrew
TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES;
FILE REFERENCE: UCO67.004A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US/10/000,439
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 09/847,208
PRIOR PILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
I DAYMOND: 1
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100.0%; Pred. No. 1.7e-92;
tive 0; Mismatches 0;
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FEATURE:
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LENGTH: 569
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Fublication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: SAXON, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
ITILE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
ITILE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
ITILE OF INVENTION: TGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UG67.002A
CURRENT APPLICANTON NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEG ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1260; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e-92; Matches 232; Conservative 0; Mismatches 0;
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FILE REFERENCE: UC067.004A
CURRENT APPLICATION NUMBER: US/10/000,439
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 09/847,208
PRIOR FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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TYPE: PRT
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Patent No. USCO20133001A1
GENERAL INFORMATION:
APPLICANT: Gefter, Malcolm L
APPLICANT: Gefter, Malcolm L
APPLICANT: Joyal, John L
APPLICANT: Gosselin, Michael
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
FILE REFERENCE: PPI-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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Pred. No. 7.1e-90;
3; Mismatches 4;
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CURRENT FILING DATE: 2001-11-27
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,198
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR FILING DATE: 2000-12-20
NUMBER: OF SEQ ID NOS: 13
SEQ ID NO 10
CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: US 60/562,627
PRIOR FILING DATE: 2004-04-14
PRIOR FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
SEQ ID NO 29
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Best Local Similarity 97.0°
Matches 225; Conservative
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CRGANISM: Homo sapiens
US-09-996-357-10
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US-09-996-357-10
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Publication No. US20050226864A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Hinton, Paul R
APPLICANT: Taurushita, Naoya
FILLE OF INVENTION: Alteration of Fc-Fusion Protein Serum Half-Lives By Mutagenesis
FILE REFERENCE: 05882.0039.NPUS07
CURRENT APPLICATION NUMBER: US/10/966,673
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APPLICANT: Saxon, Andrew; TTILE OF INVENTION: FUSION MOLECULES AND METHODS FOR; TILLE OF INVENTION: TREATMENT OF IMMUNE DISEASES; FILE REFERENCE: UC067.004A; CURRENT APPLICATION WUMBER: US/10/000,439; CURRENT FILING DATE: 2001-10-24; PRIOR APPLICATION NUMBER: US 09/847,208; PRIOR FILING DATE: 2001-05-01, NUMBER OF SEQ ID NOS: 13; SOFTWARE: FASLSEQ for Windows Version 4.0; SEQ ID NO 7.
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100.0%; Pred. No. 3.2e-92;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 232; Conservative
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TYPE: PRT
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0
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APPLICANT: Month, Michael B.
APPLICANT: Mann, Michael B.
APPLICANT: Mann, Michael B.
APPLICANT: Dunstan, Colin R.
TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
FILE REPERENCE: A-604
CURRENT APPLICATION NUMBER: US/09/389,782
CURRENT FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 7.1e-90;
3; Mismatches 4; Indels (
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Publication No. US20040110929A1
GENERAL INFORMATION:
APPLICANT: Bjorn, Soren E
APPLICANT: Bjorn, Soren E
APPLICANT: Jorgensen, Rise M
APPLICANT: Jorgensen, Anker S
TITLE OF INVENTION: TF Binding Compound
FILE REFERENCE: 6455.200-US
CURRENT APPLICATION NUMBER: US/10/617,619
CURRENT PILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: Danish Application No. PA
PRIOR FILING DATE: 2002-07-12
PRIOR PILING DATE: 2002-07-12
PRIOR PILING DATE: 2002-08-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                              // Sequence 1, Application US/09389782
/ Publication No. US20030144187A1
/ GENERAL INFORMATION:
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Best Local Similarity 97.0%;
Matches 225; Conservative
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US-09-389-782-1
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US-10-761-593A-26

Sequence 26, Application US/10761593A

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Sequence 26, Application US/10761593A

Sequence 26, Application US/10761593A

Sequence 26, Application US.

Sequence 26, Application US/10761593A

APPLICANT: Sun, Bill N

APPLICANT: Sun, Cecily R

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: activities

TITLE OF INVENTION: activities
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97.2%; Score 1225; DB 4; Length 232; 97.0%; Pred. No. 7.1e-90;
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Pred. No. 7.1e-90;
3; Mismatches 4;
                                                                                       3; Mismatches
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al Similarity 97.0%;
225; Conservative 3
                                               Best Local Similarity 97.0
Matches 225; Conservative
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Best Local Similarity
Matches 225; Conserva
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US-10-831-622-97
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RESULT 14

US-10-800-449-26

Sequence 26, Application US/10800449

Publication No. US20040265973A1

GENERAL INFORMATION:

APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: increased biological activities

TITLE OF INVENTION: increased biological activities

FILE REPERENCE: 036UN2001

CURRENT FILING DATE: 2004-03-15

PRIOR PILING DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO 26

LENGTH: 232
          121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
TITLE OF INVENTION: OF TRANSPLANT REJECTION
TITLE REPERENCE: TSR 1810.2; CURRENT APPLICATION NUMBER: US/10/964,215
CURRENT FILING DATE: 2004-10-12; PRIOR PELLORION NUMBER: US 10/831,622
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2003-04-30; NUMBER OF SEQ ID NOS: 113
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 113
                                                                                                            PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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ORGANISM: Homo sapiens
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US-10-964-215-97
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| Publication No. US20040259209A1
| GENERAL INFORMATION:
| APPLICANT: Sun, Lee-Hwei K
| APPLICANT: Sun, Eell K
| TITLE OF INVENTION: Increased biological activities
| TITLE OF INVENTION: Increased biological activities
| TITLE OF INVENTION: Increased biological activities
| TITLE OF INVENTION: UNMBER: US/10/800,497
| TITLE OF INVENTION: UNMBER: US/10/800,497
| TITLE OF INVENTION: UNBER: US/10/800,497
| TITLE OF INVENTION: UNBER: US/10/800,497
| TITLE OF INVENTION: UNBER: US/10/968,362
| PRIOR APPLICATION NUMBER: US/09/968,362
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APPLICANT: Wilkinson, Beverley
TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: TSRI 810.1
CURRENT APPLICATION NUMBER: US/10/831,622
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/467,206
PRIOR FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 113
SSGTWARE: PASISEQ for Windows Version 4.0
SSG IN 097
LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1225; DB 5;
Pred. No. 7.1e-90;
3; Mismatches 4;
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Best Local Similarity 97.0%;
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-831-622-97
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US-10-800-497-26
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Query Match 97.2%; Score 1225; DB 5; Length 232; Best Local Similarity 97.0%; Pred. No. 7.1e-90; Matches 225; Conservative 3; Mismatches 4; Indels (
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Search completed: February 22, 2006, 22:03:09 Job time : 119.604 Becs

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Sequence 7, Application US/11227340 Publication No. US20060024730A1 GENERAL INFORMATION:
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US-11-227-340-7
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USIO NEW PUB.pep:*
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(c) 1993 - 2006 Biocceleration Ltd.
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US-10-949-720-390
US-11-016-503-8
US-11-072-512-3730
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US-11-227-340-7

US-10-493-909-20

US-10-992-440-68

US-11-075-351-1

US-11-075-351-1

US-11-102-621-7

US-11-102-621-7

US-11-102-621-7

US-11-102-621-7

US-11-102-621-7

US-11-05-726-164

US-11-05-726-164

US-11-05-726-164

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US-11-173-969-6

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Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Sequence 1, Application US/10948053

Sequence 1, Application US/10948053

Sequence 1, Application US/10948053

Sequence 1, Application Occidention of US20060019887A1

GENERAL INFORMATION:

TITLE OF INVENTION: Compositions and Methods for the Prevention or Treatment of Cancrities Reference: A-605

CURRENT APPLICATION NUMBER: US/10/948,053

CURRENT FILING DATE: 2004-09-22

FRIOR TILING DATE: CURRENT APPLICATION NUMBER: US/09/389,545

FRIOR FILING DATE: CURRENT APPLICATION NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 232
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Sequence 4, Appli
Sequence 71, Appl
Sequence 121, App
Sequence 132, Appl
Sequence 70, Appl
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97.0%; Pred. No. 1.7e-101;
tive 3; Mismatches 4;
US-11-139-499-4
US-11-139-499-12
US-11-139-499-12
US-11-022-289-8
US-11-022-289-8
US-11-022-289-6
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US-11-02-289-6
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US-11-02-621-11
US-11-102-621-121
US-11-102-621-132
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Best Local Similarity 97.0
Matches 225; Conservative
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CRGANISM: Homo sapiens
US-10-948-053-1
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80 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 139
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Pred. No. 2.6e-101;
3; Mismatches 4; Indels
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Best Local Similarity 97.0%;
Matches 225; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 330
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US-10-886-383-6
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APPLICANT: Jorgensen, Anker S
TITLE OF INVENTION: TF Binding Compound
FILE REFERENCE: 6455.200-US
CURRENT APPLICATION NUMBER: US/11/227,340
CURRENT FILING DATE: 2005-09-15
PRIOR PLILING DATE: 2005-09-15
PRIOR PLILING DATE: 2003-07-11
PRIOR PLILING DATE: 2002-07-12
PRIOR PLILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/404,568
PRIOR FILING DATE: 2002-08-19
PRIOR PLING DATE: 2002-08-19
SPRIOR FILING DATE: 2002-08-19
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENTH: 232
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Pred. No. 1.9e-101;
3; Mismatches 4; Indels (
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Sequence 6, Application US/11242294
Sequence 6, Application US/11242294
GENERAL INFORMATION:
APPLICANT: Rixon, Mark W.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REFERENCE: 01-20
CURRENT APPLICATION NUMBER: US/11/242,294
CURRENT APPLICATION NUMBER: US/11/242,363
PRIOR FILING DATE: 2005-10-03
PRIOR FILING DATE: 2002-05-20
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 251
TYPE: PRI
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Best Local Similarity 97.0%;
Matches 225; Conservative 3
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US-11-242-294-6
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Sequence Application US/10886383

Publication No. US20060005571A1

GENERAL INFORMATION:

APPLICANT: Hoffmann-La Roche Inc.

TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and use:

TITLE OF INVENTION: thereof

TITLE OF INVENTION: thereof

TITLE OF INVENTION: thereof

CURRENT PILING DATE: 2004-07-08

PRIOR PRILING DATE: 2004-07-08

PRIOR APPLICATION NUMBER: EP 03015526

PRIOR APPLICATION OF 3.2
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Sequence 20, Application US/10493909

Publication No. US20060015969A1

Publication No. US20060015969A1

APPLICANT: LARRICK, JAMES W.

APPLICANT: LARRICK, JAMES W.

APPLICANT: WYGOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY

TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES

FILE REFERENCE: 41514-20004.01

CURRENT FILING DATE: 2004-04-26

PRIOR APPLICATION NUMBER: 9C7/US01/13932

PRIOR PLING DATE: 2000-04-28

PRIOR PLING DATE: 2000-04-28

PRIOR PLING DATE: 2000-04-28

WUMBER OF SEQ ID NOS: 101

SOFTWARE: PATENTIN Ver. 2.1
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                                    140 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 199
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158

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219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
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APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR APPLICATION NUMBER: US 60/531,752
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO 11
LENGTH: 330
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Publication No. US20050260716A1

GENERAL INFORMATION:
APPLICANT: MOOIE, Margaret D.
TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
FILE REFERENCE: 02-16
CURRENT FILING DATE: 2005-03-08
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1.6
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97.0%; Pred. No. 2.6e-101;
tive 3; Mismatches 4;
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Best Local Similarity 97.0
Matches 225; Conservative
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Best Local Similarity 97.0
Matches 225; Conservative
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                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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US-11-075-351-1
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; Sequence 68, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; TITLE OF INVENTION NUMBER: US/10/982,440
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT APPLICATION NUMBER: 5004-11-04
; PRIOR PILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 215
; SEQ ID NO 58 PATENTION OF SEQ ID NOS: 215
; SEQ ID NO 68
; LENGTH: 330
                                                                                                           Query Match 97.2%; Score 1225; DB 6; Length 330; Best Local Similarity 97.0%; Pred. No. 2.6e-101; Matches 225; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.2%; Score 1225; DB 6; Length 330; Best Local Similarity 97.0%; Pred. No. 2.6e-101; Matches 225; Conservative 3; Mismatches 4; Indels
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Publication No. US20050249723A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                         ; ORGANISM: Homo sapiens
US-10-493-909-20
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US-10-982-440-68
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US-11-022-289-11
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218

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APPLICANT: Protein Design Labs, Inc.
APPLICANT: Hinton, Paul R.
APPLICANT: Hinton, Paul R.
APPLICANT: Tsuruabita, Naoya
APPLICANT: Tsuruabita, Naoya
APPLICANT: Tsuruabita, Naoya
APPLICANT: Tsuruabita, Naoya
APPLICANT: Vasquez, Maximilliano
TITLE OF INVENTION: ALTERATION OF FCRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ALTERATION OF FCRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ALTERATION NUMBER: US/11/102,621
CURRENT FILING DATE: 2005-04-08
PRIOR FILING DATE: 2004-04
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 EPKSCOKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158
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97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels
                                                                                                               Length 330;
                                                                                                            Score 1225; DB 7;
Pred. No. 2.6e-101;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
                                                                                                                 97.2%;
97.0%;
                                                                                                                    Query Match
Best Local Similarity 97.0°
Matches 225; Conservative
                                          , ORGANISM: Homo sapiens
US-11-102-621-3
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ORGANISM: artificial
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Publication No. US20050276799A1
GENERAL INFORMATION:
APPLICANT: Frortein Design Labs, Inc.
APPLICANT: Frortein Brown
APPLICANT: Tructubitta, Naoya
APPLICANT: Tsuchitta, Naoya
APPLICANT: Tsuchitta, Naoya
APPLICANT: Tsuchitta, Naoya
APPLICANT: Vasquez, Maximilitano
TITLE OF INVENTION: ALTERATION OF FCRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05802.0039.00PC03
CURRENT APPLICATION NUMBER: US/11/102,621
CURRENT FILING DATE: 2005-04-08
PRIOR FILING DATE: 2004-04-09
PRIOR FILING DATE: 2004-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPFRKDTLMISKIPEVTCVVVDVSHEDPEVKF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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279 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNYTQKSLSLSPGK 330
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97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels (
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Novak, Julia E.
APPLICANT: Novak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFERENCE: 00-108
CURRENT APPLICATION NUMBER: US/11/165,141
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/09/995,898
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR FILING DATE: 20001-11-28
PRIOR PILING DATE: 20001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastESQ for Windows Version 3.0
LENGTH: 330
                                                                                                                         S-11-165-141-15
Sequence 15. Application US/11165141
Publication No. US20050266485A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 3
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US-11-165-141-15
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121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNCQPENNYKTTP 180
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Sequence 1, Application US/11233683

Publication No. US20060025573A1

GENERAL INFORMATION:

APPLICANT: Gillies, Stephen

TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins

TITLE REFERENCE: LEX-017

CURRENT APPLICATION NUMBER: US/11/233,683

PRIOR PILING DATE: 2005-09-23

PRIOR PILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin version 3.0
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) OTHER INFORMATION: human Ig gamma heavy chain C region
US-11-233-683-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.2%; Score 1225; DB 7; Best Local Similarity 97.0%; Pred. No. 2.6e-101; Matches 225; Conservative 3; Mismatches 4;
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PRIOR APPLICATION NUMBER: US 60/626,991
PRIOR FILING DATE: 2004-11-10
PRIOR PLING DATE: 2004-11-12
PRIOR FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US 10/822,231
PRIOR FILING DATE: 2004-03-26
PRIOR FILING DATE: 2003-09-26
PRIOR FILING DATE: 2003-09-26
PRIOR PLING DATE: 2003-09-36
PRIOR FILING DATE: 2003-03-03
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 11
SOFWARE: Patentin version 3.3
SEQ ID NO LEBORTH: 330
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain ; OTHER INFORMATION: constant region US-11-005-726-164
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                                                                                                                                                                  APPLICANT: RELEGIONATION, ACCUI.
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REPERENCE: MER-131
CURRENT APPLICATION NUMBER: US/11/005,726
CURRENT PILING DATE: 2004-12-07
PRIOR FILING DATE: 2004-05-10
PRIOR FILING DATE: 2002-11-11
PRIOR FILING DATE: 2002-11-11
PRIOR FILING DATE: 2001-11-12
NUMBER OF SEQ ID NOS: 165
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 164
LENGTH: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.2%; Score 1225; DB 7;
97.0%; Pred. No. 2.6e-101;
tive 3; Mismatches 4;
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APPLICANT: Dang, Wei
APPLICANT: Desjarlais, John R.
APPLICANT: Marki, Sher Bahadur
APPLICANT: Vafa, Omid
APPLICANT: Hayes, Robert
TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REFERENCE: A-71386-9
CURRENT APPLICATION NUMBER: US/11/124,620
CURRENT APPLICATION NUMBER: US 60/569,440
PRIOR APPLICATION NUMBER: US 60/569,400
PRIOR APPLICATION NUMBER: US 60/569,906
PRIOR PILING DATE: 2004-07-15
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
                                                                           Sequence 164, Application US/11005726
Publication No. US20060018903A1
GENERAL INFORMATION:
APPLICANT: HELLENDOORN, Koen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/11124620
Publication No. US20060024298A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 97.0
Matches 225; Conservative
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US-11-124-620-1
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Sequence 35, Application US/11024251
Publication No. US20050266425A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
APPLICANT: Paris, Mark
TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
FILE REPRENCE: 1843.0230001
CURRENT APPLICATION NUMBER: US/11/024,251
FRIOR APPLICATION NUMBER: 60/533,241
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.3
SEQ ID NO 35
LENGTH: 335
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164 NWYVDGVEVHNAKTKPREEQ?NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 335;
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97.2%; Score 1225; DB 7;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: IGG Secreted Constant Domain US-11-024-251-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 22, 2006, 22:03:44 Job time : 12.0207 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                              RESULT 15
US-11-024-251-35
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February 22, 2006, 21:24:11; Search time 152.263 Seconds (without alignments) 669.475 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Spi nemin 1966s	Нишап	GE2 fu	Adz87506 Human IgG	Adz69628 Human IgG	Aaw26232 Human IgG	Aab28690 Human IgG	Aab80897 Human IgG	Aay72915 Human par	Aae15347 Human imm	Aae26272 Human IgG	Herpes	Human	Human	Adu51146 Human spl	Adw39127 Novel TNF	Adv91799 Human GCS	Adv99720 Human 1gG	Ady55884 Human IgG	Human	Aea18941 Human IgG	Aea88761 Human IgG	Abb09463 Human IgG	Ady22146 Human imm
SUMMARIES	ΙD	AAO19665	AA019664	AA019668	ADZ87506	ADZ69628	AAW26232	AAB28690	AAB80897	AAY72915	AAE15347	AAE26272	ADJ65991	ADJ57512	ADR48992	ADU51146	ADW39127	ADV91799	ADV99720	ADY55884	AD286538	AEA18941	AEA88761	ABB09463	ADY22146
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Abj38647 pCXFc pro	Ada89055 Plasmid p	Add25647 Binding d	Adg74307 Fibroblas	Ady21627 Human IgG	Aae26274 Human bet	Abb81490 Human imm	Aae35214 Human wil	Aay24154 Protein f	Aae26273 Human tPA	Adj52120 CH1 delet		Aab47590 Fusion pr	Aea89541 Human imm	Aar91806 Human imm	Adp56389 Human PRO	Ads82579 Human IgG	Aab04071 Zcytor 10	Aam47856 Human Ig-	Aae21960 Human dea	Abb81641 Human IgG
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## ALIGNMENTS

AA019665 standard; protein; 232 AA.

RESULT 1 AAO19665 ID AAO1

New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases. Human; IgG1; immunoglobulin G; immunotherapy; immune disease; Fcepsilon receptor; autoimmune disease; constant region; heavy chain; antiasthmatic; antiallergic; antialfammatory; dermatological; antiathritic; antirheumatic; antidiabetic; neuroprotective; Human IgG1 heavy chain constant region hinge-CH2-CH3 portion. 01-MAY-2002; 2002WO-US013527 01-MAY-2001; 2001US-00847208. 24-OCT-2001; 2001US-00000439. ä (first entry) (REGC ) UNIV CALIFORNIA. Zhang K, Zhu hinge-CH2-CH3 region WPI; 2003-103456/09. WO200288317-A2. 28-MAR-2003 Homo sapiens. 07-NOV-2002. AA019665; Saxon A, 

Claim 19; Fig 3; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypoptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypoptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FeepsilonR). Also provided are nucleotide sequences encoding such a

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            treating an igg-mediated biological response, preferably an igg-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, according a communitie, severe food allergies, chronic uritoaria, angloedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptomes resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgGl heavy chain constant region hinge-CH2-CH3 portion
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Fcepsilon receptor; autoimmune disease; constent region; heavy chain;
antiasthmatic; antiallergic; antiinflammatory; dermatological;
antiarthritic; antirheumatic; antidiabetic; neuroprotective.
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protein. The fusion molecules and compositions are useful for
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100.0%; Pred. No. 3.3e-91;
ive 0; Mismatches 0;
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24-OCT-2001; 2001US-00000439.
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present invention relates to a fusion molecule comprising a first

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polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FrespionR). Also provided are nuclectide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, prefrably an IgE-mediated hypersensitivity reaction, such as asthma, allegic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angloedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, crype-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgG1
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GE2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; IgE; immunoglobulin E; immunotherapy; immune disease; Pcepsilon receptor; autoimmune disease; constant region; heavy antiallergic; antiinflammatory; dermatological; antiarthritic; antifrheumatic; antidiabetic; neuroprotective;
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100.0%; Pred. No. 5.1e-91;
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24-OCT-2001; 2001US-00000439.
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                                                                                                                                                                                                                                                             Sequence 330 AA;
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polypeptide sequence capable of specific binding to a native Igg inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FcepailonR). Also provided are nuclectide sequences encoding such a cusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hippersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatities, severe food allergies, chronic uriticaria, angiosedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthrifis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a consultation immunotherapy. The present sequence is a gammahinge-CHapamma2-(Gly4Ser)3-CHepsilon3-CHepsilon3-CHepsilon3 fusion consultation in the invention (designated GE2) of the invention
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New fusion molecules comprising polypeptide sequences that bind to Ig inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoAnmune diseases.
                                                                                                                                       The present invention relates to a fusion molecule comprising a first
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                                                                                                 Claim 35; Fig 7; 116pp; English
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PROD INC.

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                                                                                                                                                                                          This invention relates to a novel MUC1 chimeric protein which comprises a first polypeptide sequence and a second polypeptide sequence, where the first polypeptide sequence is a MUC1 extracellular (MUC1-EC) polypeptide, and the second polypeptide sequence is a human immunoglobulin FC polypeptide or a human albumin polypeptide. The invention may be useful for the development of compounds with a cytostatic activity acting as MUC1 antagonists or CD227 antagonists. The MUC1 chimeric protein is useful in preparing a composition for treating cancer. The present sequence is that of a protein which was used during the development of the novel MUC1 chimeric protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain constant region; antibody engineering; protein engineering; immunoglobulin; mutein; fusion protein; cancer; cytostatic; neoplasm; autoimmune disease; immunosuppressive; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKKKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                            MUC1 ligand trap comprising a MUC1 extracellular polypeptide and an immunoglobulin FC polypeptide or an albumin polypeptide, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 232
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human IgG1 heavy chain constant region, mutant L314M.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1232; DB 9;
Pred. No. 5.4e-89;
                                                                                                                                                                                                                                                                                                                                                                                                          97.8%; Score 5.46-0
97.4%; Pred. No. 5.46-0
                                                                                                                                                              Disclosure; SEQ ID NO 33; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 97.4
Matches 226; Conservative
               Kufe DW;
                                             WPI; 2005-346855/35.
                                                              N-PSDB; ADZ87507
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 232 AA;
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               Kharbanda S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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AAW26232 Btandard; protein; 232

AAW26232

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the invention tradece to a mountained religions delected from cesidues 250, 314, and 428 (Kabat numbering) is different from that residues 250, 314, and 428 (Kabat numbering) is different from that comprising an PC residon protein. Also included are an FC fusion protein comprising an PC residon substantially identical to that of the corresponding unmodified FC-fusion protein.

Consisting of the corresponding unmodified FC-fusion protein a modified for residues 250, 314, and 428 is different from the propertion where at least one amino acid residue selected from the group consisting of residues 250, 314, and 428 is different from the present in the unmodified IgG class antibody), an isolated polynucleotide in the unmodified IgG class antibody), an isolated polynucleotide conjugation or polymetrial to a sequence selected from ADZ69600-ADZ69656, an isolated comprising an amino acid sequence at least 90% identical to a sequence selected from ADZ69600-ADZ69656, an isolated comprising at least one amino acid sequence at least 90% identical to binding affinity/serum half-life of an PC-fusion protein (comprising selecting at least one amino acid residue as cited above, and confirmed present in the PC-fusion protein) and a method for producing at modified PC-fusion protein) and a method of producing an entire present in the PC-fusion protein) and a method of producing an entirely for propertial properties of properties of producing an entirely for present in the PC-fusion protein) and a method of producing an entirely for properties of producing an entirely for properties of producing an entirely for protein protein with an altered binding affinity for present in the present with an altered binding affinity for properties of producing an entirely for protein protein when an altered binding affinity for present and protein which an altered binding affinity for properties of producing and protein protein when an altered binding affinity for properties of producing and protein protein protein form protein protein protein p
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                                                                                                                                                                                                                                                                                          New modified Fc-fusion protein where at least one amino acid residue from the heavy chain constant region, useful for studying protein function in vitro and in vivo and as potential therapeutic and diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to a modified Fc-fusion protein where at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; SEQ ID NO 29; 170pp; English
                                                                                                 (PROT-) PROTEIN DESIGN LABS INC.
15-OCT-2003; 2003US-0511687P.
14-APR-2004; 2004US-0562627P.
                                                                                                                                                                   TBurushita N;
                                                                                                                                                                                                                                  WPI; 2005-315683/32.
                                                                                                                                                                   Hinton PR,
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                                                                                  NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                     ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                             Gaps
                                                                                                                                                                                                                                    PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                  Score 1228; DB 9; Length 330;
Pred. No. 1.7e-88;
2; Mismatches 4; Indels (
                       97.5%;
97.4%;
                                  Best Local Similarity 97.4
Matches 226; Conservative
Sequence 330 AA;
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                                                                                                                                                                                                  219
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                       Query Match
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A novel recombinant vector has been developed which comprises a nucleotide sequence encoding a fusion protein. The fusion protein comprises three domains joined together in order, from N-terminus to C-terminus, of a first domain comprising a protein of interest, a second domain comprising a hydrophilic spacer and an affinity domain, each domain comprising amino acid residues. The present sequence represents the hinge/Fr region of human IgG1, used in example 3 of the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention is useful for the expression of fusion proteins capable of isolation by affinity of the order of the production of authentic proteins of interest the efficient cleavage and generation of authentic proteins of interest that do not contain extraneous (i.e. non-naturally occurring) amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant protein expression system for fusion protein production - useful for high quantity production of authentic recombinant proteins.
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                                                                                                             Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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97.0%; Pred. No. 1.9e-88;
iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 133-134; 194pp; English.
                                                                                                                                                                                                                                                                                       96US-00595043.
                                                                                                                                                                                                                                                        97WO-US001470.
                                                                                       Human IgG1 hinge/Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                      (TECH-) TECHNOLOGENE INC
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-402624/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT80158
                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                      31-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                  Sgarlato GD;
                                                                                                                                                                                                                             07-AUG-1997.
                                                          16-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence was used in the production of AGP-1 fusion proteins. AGP-1 is a type II transmembrane protein. The fusion proteins comprise an Pc immunoglobulin region fused to the N-terminal portion of the AGP-1 and protein. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-breast, prosites. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies
                                                                                                                                                                                                                                                                                             Human; AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
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                                                                                                                                                                                                                        Human IgGgammal hinge, CH2 and CH3 regions.
AAB28690 standard; protein; 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 1; 93pp; English.
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                                                                                                                                                  (first entry)
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                                                                                                                                                  14-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypoptide or OPG fusion protein. The OPG proteins (see AAB80898-AAB80905) can inhibit formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The present sequence is the hinge. CH2 and CH3 regions of human 1g9gammal. This sequence can be used to generate fusion proteins of OPG and immunoglobulin, for use in the present invention. The generated fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for the prevention or treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preventing or treating lytic bone diseases, particularly associated w cancer or metastasis, by administering an osteoprotegrin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                 Human; IgGgammal; anticancer; Antimetastatic; Osteogenic; lytic bone disease; multiple myeloma; immunoglobulin, osteosclerotic bone metastasis; OPG; osteoprotegrin, osteoclar formation inhibition; bone resorbtion inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 232;
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97.0%; Pred. No. 1.9e-88;
iive 3; Mismatches 4;
                                                                                                                                                                                                   Human IgGgammal hinge, CH2 and CH3 regions.
AAB80897 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 87pp; English.
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                                                                                                                                    (first entry)
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Matches 225; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                    31-MAY-2001
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                                                                     AAB80897;
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AAE15347 standard; protein; 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses fusion protein comprising human osteoprotegerin (OPG) protein fused by linker to human 1961 Rc portion. OPG negatively regulates formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion protein is administered for the reabsorption of bone. The OPG-Fc fusion protein is administered for osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic lossening. The present sequence is partial human immunoglobulin G (1g G) locening. The present sequence is partial human immunoglobulin G (1g G) Hrotein comprising the hinge and heavy chain constant regions CH2 and CH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, fusion protein; osteoprotegarin; OPG; Pc protein; osteopathic; therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis; hypercalcaemia; osteopenia; osteonecrosis; rheumatoid archritis; osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1; periodontal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                   Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.
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Pred. No. 1.9e-88;
3; Mismatches 4
      standard, protein, 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mann MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 1; 119pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.2%;
97.0%;
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                                                                                                                                                                                                                                                                                                                                                                     99US-00389782
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Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunstan CR, Wooden SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-244572/25.
                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                     WO200118203-A1.
                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                     03-SEP-1999;
                                                                       13-JUN-2001
                                                                                                                                                                                                                                                                                                     15-MAR-2001
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                                       AAY72915;
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The invention relates to a method for increasing and maintaining content in a mammal. The method comprises administering a had all the process, and the invention in a mammal. The method comprises administering a composition, less frequently than an equivalent molar amount of and at a composition, less frequently than an equivalent molar amount of and at a lower molar amount than recombinant human Epo (rHuEpo) to obtain a comparable target haematocrif. Epo is a glycoprotein hormone necessary for the maturation of erythroid progenitor cells into erythrocytes. Human Epo comparable target haematocrif in a mammal suffering from anaemia associated with a decline or loss of kidney function, myelosuppressive therapy comprising chemotherapeutic or anti-viral drugs or associated with a present sequence is human immunoglobulin G (IgG) gamma 1 constant heavy chain (CH2) (CH3) hinge region used to construct Epo hyperglycosylated analogue fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing and maintaining hematocrit in mammal suffering from anemia, comprising administering hyperglycosylated analog of erythropoietin less frequently and at lower molar amount of recombinant human erythropoietin.
                                                  Human; erythropoletin; Epo; haematocrit; anaemia; kidney function; IgG; cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.
Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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97.0%; Pred. No. 1.9e-88;
iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sitney KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Browne JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 10; 95pp; English.
                                                                                                                                                                                                                                                                                                                                              19-APR-2001; 2001WO-US012836.
                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-00559001
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Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elliott SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-034433/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
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                                                                                                                                                               Ното варіелв.
                                                                                                                                                                                                                                                                                 01-NOV-2001
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RESULT 11

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The invention relates to a compound comprising an immunoglobulin (Ig)
heavy chain constant region or its fragment that retains the ability to
bind an Fo receptor linked by a linker group or a direct bond to a
c peptide capable of binding an amyloidogenic protein. The invention is
useful for clearing an amyloidogenic protein The invention is
c useful for clearing an amyloidogenic protein The invention is
c useful for clearing an amyloidogenic protein such as beta-amyloid,
c transthyretin (TTR), prion protein (PPP), islet amyloid, polypeptide
c (TAPP), atrial natriuretic factor (AMP), kappa light chain, lambda light
c thain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I,
c (App), atrial natriuretic factor (AMP), kappa light chain, lambda light
c chain, amyloid A, procalcitonin, fibrinogen, Huntington, alpha-synuclein and
lysozyme from a subject and for tracting an amyloidogenic disorder such
as Alzheimer & disease and spongiform encephalopathy. Disorders treatable
amyloid cardiomyopathy), PPP (eg. spongiform encephalopathies, including
acrapie in sheep, bovine spongiform encephalopathy in cows and
creutzfeldt-Jacob disease (CJ) and Gerstmann-Straussler-Scheinker
syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),
ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg.
c diopathic amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal
amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis), Gelsolin (eg.
c tammloidosis), Lysozyme (eg. hereditary systemic amyloidosis),
amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis),
c used in the exemplification of the invention
                                                                                                                                                                                              Human, amyloidogenic protein, Alzheimer's disease, Huntington's disease, spongiform encephalopathy, familial amyloid cardiomyopathy; amyloidosis, Gerstmann-Straussler-Scheinker syndrome, spongiform encephalopathy, GSS; Creutzfeldt-Jacob disease, insulinoma, diabetes, body myocytis, myeloma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel therapeutic agent useful for treating an amyloidogenic disorder, e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain constant region linked to a peptide capable of binding amyloidogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.2%; Score 1225; DB 5; Length 232; 97.0%; Pred. No. 1.9e-88; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gosselin M;
                  AAE26272 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Page 76; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Israel DI, Joyal JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-2000; 2000US-0253302P.
29-NOV-2000; 2000US-0250198P.
20-DEC-2000; 2000US-0257186P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2001; 2001WO-US044581.
                                                                                                         14-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                      Human IgGl heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-636427/68.
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                                                                                                                                                                                                                                                                                                                                                                                   WO200242462-A2.
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gefter ML,
                                                               AAE26272;
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AAE26272
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New therapeutic agent, useful for treating endotoxin induced disease, comprises fusion protein of Herpes virus entry mediator protein and
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                                                                                                                    Claim 5; SEQ ID NO 2; 11pp; Japanese.
N-PSDB; ADJ65998.
                                                                                                                                                                                                                                                                                                                             Sequence 232 AA;
                                                                                immunoglobulin.
                                                                                                                                                                                                                                                                                     specification.
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The compound (I) has the formula A-(LM)-C, where A is a FVIIa polypeptide, LM is an optional linker group, C comprises an optional linker group, C comprises an modification of the manufacture of a medicament for linhibits TF-medicament, and for the manufacture of a medicament for preventing or treating disease or disorder associated with pathophysiological TF activity. The disease or disorder associated with pathophysiological TF activity are deep venous thrombosis, arterial thrombosis, post surgical thrombosis, coronary artery bypass graft (PAGG), percutaneous transdermal coronary angioplastry (PTGA), stroke, cancer, tumor metastasis, angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis, angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis, andiodericosis and restences following angioplastry, acute and chronic indications such as inflammation, septic shock, septicemia, hypotension, adult respiratory distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial infarction, or prophylactic treatment of mammals with atherosclerotic vessels at risk for thrombosis. The present sequence represente the Fc domain fragment of human immunoglobulin GI (19G1).
                                        ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic; cerebroprotective; cytostatic; vasotropic; antihumanic; antiarthritic; antitateriosclerotic; antiin[ammatory; antibacterial; immunosuppressive; hypertensive; cardiant; coagulation Factor VII; human; immunoglobulin G1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compound binding to tissue factor, useful for treating diseases such inglogenesis, ischemia/reperfusion, and rheumatoid arthritis.
                                                                                                                                      PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                               PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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97.0%; Pred. No. 1.9e-88;
tive 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; SEQ ID NO 7; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           ADJ57512 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IgG1 Fc domain fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-2003; 2003WO-DK000481.
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Best Local 8
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(HUEPD), a peptide linker, and a human IgG Fc variant, is new.

(HUEDD), a peptide linker, and a human IgG Fc variant, is new.

(HUEDD), a peptide linker and a human IgG Fc variant, is new.

(INDEDENDENT CLAIMS are also included for the following: a chinese hamster ovary (CHO)-derived cell line producing the HUEDO-L-vFc fusion procein in its growth medium in excess of 10 Emicro; per million cells in a 24 hour period; an entend for making a recombinant fusion protein comprising HUEDO, a flexbble peptide linker, and a human IgG Fc variant. Preferred Protein: The peptide linker containing 20 or fewer amino acids is present between HUEDO and the human IgG Fc variant, alanine, and threonine. The human IgG Fc variant, serine, alanine, and threonine. The human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human IgG Variant comprises a hinge, CH2, and CH3 domains of human IgG Variant and Leucl35Ala mutations comprising 437 amino acids (SEQ ID NO. 18). It further comprises a hinge, CH2, and CH3 domains of human IgG I with Leucl34Aul, Leucl35Ala mutations comprising 437 amino acids (SEQ ID NO. 22). The HUEPO-L-VFC fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant HuBPO-L-vFc fusion protein comprises human erythropoietin (HuBPO), a peptide linker, and a human IgG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis.
                                                                                ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antianaemic; nephrotropic; human; HuBPO-L-vFc; erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis; AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                          PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IgG1 hinge and CH2 region.
                                                                                                                                                                                                                                                                                                                                                           ADR48992 standard; peptide; 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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(SUNB/) SUN B N C.
(SUNC/) SUN C R Y.
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4; Indels

Best Local Similarity 97.0 Matches 225; Conservative

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29-APR-2004; 2004WO-EP004562 30-APR-2003; 2003US-0467206P

402004096976-A2 11-NOV-2004. (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS PHARMA G! (SCRI ) SCRIPPS RES INST.

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CC 30 & Amicro; gper million cells in a 24 hour period. The human IgG FC variant comprises a hinge, CH2, CH3 domains of human IgG FC variant comprises a hinge, CH2, CH3 domains of human IgG FC variant comprises a hinge, CH2, CH3 domains of human IgG FC variant comprises a hinge, CH2, CH3 domains of human IgG FC variant comprises a hinge, CH3, EG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, IgG2 as SEQ ID NO. 18, and IgG4 as Preferred Method: Making a recombinant CC that of rhuBPO on a molar basis. Preferred Method: Making a recombinant CC that of rhuBPO on a molar basis. Preferred Method: Making a recombinant CC cell line where the recombinant protein is expressed in its growth medium in excess of 10 & Amicro; gp er million cells in a 24 hour period; and CC protein exhibits in vitro biological activity similar to or higher than CC that of rhuBPO on a molar basis. Antianemic; Nephrotropic. No biological activity similar to or higher than ctravenous route. No dosage given. The recombinant HuBPO-L-vFc fusion protein is useful for treating patients with chronic anemia due to renal diseases, cancer chemocherapy, rheumatoid architists, AZT treatment for treatment of remain failure. A fusion protein was assembled from several DNA segments. To obtain the gene encoding the leader peptide and mature CC brotein of human erythropoletin (EPO), cDNA library of human erythropoletin served as the resulting DNA fragmen
   Preferred CHO-Derived Cell Line:
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Sequence 232 AA;

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                                                                                                                                    61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                       61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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                                                                  1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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Ouery Match 97.2%; Score 1225; DB 8; Length 232; Best Local Similarity 97.0%; Pred. No. 1.9e-88; Matches 225; Conservative 3; Mismatches 4; Indels (
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ADU51146 standard; protein; 232 AA. 27-JAN-2005 (first entry) ADU51146; 

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Job time : 155.263 secs

Human spleen-expressed receptor-related solubility-promoting protein.

immunosuppressive, cytostatic, antiinflammatory, immune modulation, intercellular communication, autoimmune disease, cancer, neoplasm; transplant rejection, immune disorder; inflammation; gene therapy.

Homo sapiens

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                New purified spleen expressed (SPEX) polypeptide useful for modulating lymphocyte activation and the immune response in disorders including autoimmunity, cancer, transplant rejection and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NWYVDGVEVHNAKTIKPREEQYNSTYRVVSVLIVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solubility-promoting protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 97; 98pp; English.
                                                                                                                                                                                                                                   Kaye J, Wilkinson B;
                                                                                                                                                                                                                                                                           WPI; 2004-804740/79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 232 AA;
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